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RX RA
RA Bosma P.J., van den Berg E.A., Koosstra T., Siemieniak D.R.,
RA Slightom J.L.; "Human plasminogen activator inhibitor-1 gene. Promoter and structural gene nucleotide sequences.";
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RN Mottonen J., Strand A., Smersky J., Sweet R.M., Danley D.E.,
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RN RX
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RN Nature 355:270-273(1992).
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RN Structure 6:627-636(1998).
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RN RX
RN MEDLINE=99148119; PubMed=10368279; DOI=10.1016/S0969-2126(99)80018-5;
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
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RP TISSUE-LUNG; MEDLINE=2388857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RN RX
RA Strasberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Richards K.C., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Panay J., Heitton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green F.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.F., Jones S.J.M., Marra M.A.,
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RN MEDLINE=86311660; PubMed=3032219;
RN NY T., Sawdaye M., Lawrence D., Millan J.L., Loskutoff D.J.; "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor.";
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[13] NUCLEOTIDE SEQUENCE OF 1-47 AND 364-402. RP ERERATUM.
RN MEDLINE=87080762; PubMed=305016; DOI=10.1016/0014-5793(86)81113-9;
RA Andreassen P.A., Riccio A., Welinder K.G., Douglas R., Sartorio R.,
RA Nieles L.S., Oppenheimer C., Blasi F., Danoe K.; "Plasminogen activator inhibitor type I: reactive center and amino-terminal heterogeneity determined by protein and cDNA sequencing.";
RT RT RN
RN PERS Lett. 209:213-218(1986).
[14] NUCLEOTIDE SEQUENCE OF 17-402, AND PARTIAL PROTEIN SEQUENCE. RP INERACTION WITH LRPIB.
RN MEDLINE=21368943; PubMed=11384978; DOI=10.1074/jbc.M10227200;
RA Liu C.-X., Li Y., Obermeier-McCormick L.M., Schwartz A.L., Bu G.,
RC Tissue=Placenta;
RX MEDLINE=87105925; PubMed=3026837; DOI=10.1016/0014-5793(87)81288-7;
RT "The putative tumor suppressor LRPIB, a novel member of the low

DR Pfam; PF00079; Serpin; 1.	RN NUCLEOTIDE SEQUENCE OF 153-235.
DR PROSITE; PS00284; SERPIN; 1.	RP Adrenal cortex;
KW Glycoprotein; Plasma; Plasminogen activation; Protease inhibitor;	RC TISSUE=Adrenal cortex;
KW serine protease inhibitor; Serpin; Signal.	RC MEDLINE=0338128; PubMed=1696269; DOI=10.1083/jcb.111.2.743;
FT SIGNAL 1 23 By similarity.	RA Pepper M. S., Belin D., Montesano R., Orci L., Vassalli J.-D.,
FT CHAIN 24 402 Plasminogen activator inhibitor-1.	RT "Transforming growth factor-beta 1 modulates basic fibroblast growth
FT SITE 369 370 Reactive bond.	RT factor-induced proteolytic and angiogenic properties of endothelial
FT CARBOHYD 232 232 N-linked (GlcNAc . .) (Potential).	RT cells in vitro.";
FT CARBOHYD 288 288 N-linked (GlcNAc . .) (Potential).	RL J. Cell Biol. 111:743-755(1990).
FT CARBOHYD 352 352 N-linked (GlcNAc . .) (Potential).	CC FUNCTION: This inhibitor acts as "bait" for tissue plasminogen
SEQUENCE 402 AA; 45450 MW; 13650E5F4F8FB405 CRC64;	CC activator, urokinase, and protein C. Its rapid interaction with
	CC TPA may function as a major control point in the regulation of
	CC fibrinolysis.
Query Match Score 1790; DB 1; Length 402;	CC SUBUNIT: Interacts with vtn. Binds LRPIB; binding is followed by
Best Local Similarity 86.3%; Pred. No. 1.9e-135;	CC internalization and degradation. (By similarity).
Matches 347; Conservative 26; Mismatches 29; Indels 0; Gaps 0;	CC SUBCELLULAR LOCATION: Secreted.
Qy 1 M Q M P S A L T V C L V G A L V F G C G S A V H P P S Y V A H L A S D F G V R V F Q Q A Q A S K D R N V V F S P Y 60	CC TISSUE SPECIFICITY: Vascular endothelial cells may be the primary
Db 1 M R M S L V F A C I A M G L A L T F A G S A S S H H Q S L A A R L T A F G V R V F Q V D V Q A S K D R N V V F S P Y 60	CC site of synthesis of plasma PAI.
Qy 61 G V A S U L A M I L O L T G G E T Q O Q I Q A M G K P I D D K G M A P A I R H Y K E L M G P N K D E I S T D A I 120	CC SIMILARITY: Belongs to the serpin family.
Db 61 G V A S V L A M I L O L T G G E T Q O Q I Q A M G K P I D D K G M A P A I R H Y K E L M G P N K D E I S T D A I 120	CC SwISS-Prot entry is copyright. It is produced through a collaboration
Qy 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180	CC the European Bioinformatics Institute. There are no restrictions on its
Qy 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180	CC use as long as its content is in no way modified and this statement is not
Db 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180	CC removed.
Qy 181 D Q L T R L V L V N A L Y F N G Q M K T P F P D S S T H R L F H K S D G S T V S V P M A Q T K N F Y T E F T T P D 240	CC EMBL; X16383; CAA34419.1; -; mRNA.
Db 181 D Q L T R L V L V N A L Y F N G Q M K T P F P D S S T H R L F H K S D G S T V S V P M A Q T K N F Y T E F T T P D 240	CC EMBL; X52906; CAA37094.1; -; mRNA.
Qy 181 D Q L T R L V L V N A L Y F N G Q M K T P F P E S T H R L F H K S D G S T V S V P M A Q T K N F Y T E F S T D 240	CC PIR; S06745; S06745.
Db 181 D Q L T R L V L V N A L Y F N G Q M K T P F P E S T H R L F H K S D G S T V S V P M A Q T K N F Y T E F S T D 240	CC HSSP; P05121; 9 PAI.
Qy 241 G H Y D I L E D P Y H G D T L S M F I A A P Y K E V P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K 300	CC InterPro; IPR000215; Prot_inh_Serpin; 1.
Db 241 G H Y D I L E D P Y H G D T L S M F I A A P Y K E V P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K 300	CC PANHER; PTM11461; Prot_Inh_Serpin; 1.
Qy 301 F S L E P D V D L K P L E N G M T M F Q Q A D F T S L D E P L H A V A Q A L O K V K I E V N E S G T V A S S 360	CC PROSITE; PS00284; SERPIN; 1.
Db 301 F S L E P D V D L K P L E N G M T M F Q Q A D F T S L D E P L H A V A Q A L O K V K I E V N E S G T V A S S 360	CC DR Direct protein sequencing; Glycoprotein; Plasma;
Qy 361 S T A V I V S A R M A P E E I I M D R P F L F V T R H N P T G V L F M G Q M E P 4 0 2	CC KW Plasminogen activation; Protease inhibitor; Serine protease inhibitor;
Db 361 S T A V I V S A R M A P E E I I M D R P F L F V T R H N P T G V L F M G Q M E P 4 0 2	CC KW Serpin; Signal:
RESULT 4	CC SIGNAL 1 23 Plasminogen activator inhibitor-1.
PATTI_BOVIN STANDARD; PRT; 402 AA.	FT CHAIN 24 402 Reactive bond.
ID_PATTI_BOVIN	FT SITE 369 370 Best local similarity 86.3%; Pred. No. 5.9e-135;
AC_PATTI_BOVIN	FT SITE 369 370 Mismatches 30; Indels 0; Gaps 0;
DT_PATTI_BOVIN	FT SITE 369 370
DT_01-JAN-1990	FT SITE 369 370
DT_01-JAN-1990	FT SITE 369 370
DT_10-MAY-2005	FT SITE 369 370
DB_PATTI_BOVIN	FT SITE 369 370
GN_PATTI_BOVIN	FT SITE 369 370
OS_Bos_taurus	FT SITE 369 370
OC_Metazoa	FT SITE 369 370
OC_Eutheria	FT SITE 369 370
OC_Laurasiatheria	FT SITE 369 370
OC_Cetartiodactyla	FT SITE 369 370
OC_Ruminantia	FT SITE 369 370
OC_Bovidae	FT SITE 369 370
OC_Bovine	FT SITE 369 370
NCBI_TaxID_9913	FT SITE 369 370
PROTEIN_NUCLEOTIDE_SEQUENCE	FT SITE 369 370
RP_MEDLINE=00067567; PubMed=2587231;	FT SITE 369 370
RP_MEDLINE=8329072; PubMed=3262060;	FT SITE 369 370
RA_Mimuro J., Sawdey M., Hatori M., Loskutoff D.J.;	FT SITE 369 370
RT "CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1)." ;	FT SITE 369 370
RL_Nucleic_Acids_Res	FT SITE 369 370
[2] PROTEIN_SEQUENCE_OF_24-63.	FT SITE 369 370
RP_MEDLINE=8329072; PubMed=2587231;	FT SITE 369 370
RA_Katagiri K., Okada K., Hattori H., Yano M.;	FT SITE 369 370
RT "Bovine endothelial cell plasminogen activator inhibitor. Purification and heat activation.";	FT SITE 369 370
RL_Eur_J_Biochem_176:81-87(1988).	FT SITE 369 370
Query Match Score 1784; DB 1; Length 402;	Query Match Score 1784; DB 1; Length 402;
Best Local Similarity 85.3%; Pred. No. 5.9e-135;	Best Local Similarity 85.3%; Pred. No. 5.9e-135;
Matches 343; Conservative 29; Mismatches 30;	Matches 343; Conservative 29; Mismatches 30;
Qy 1 M Q M P A L T C V I G A L V G E S A V H P P S Y V A H L A S D F G V R V F Q Q A Q S K D R N V V F S P Y 60	Qy 1 M Q M P A L T C V I G A L V G E S A V H P P S Y V A H L A S D F G V R V F Q Q A Q S K D R N V V F S P Y 60
Db 1 M R M S P V F A C I A M G L A L T F A G S A S S H H Q S L A A R L T A F G V R V F Q V D V Q A S K D R N V V F S P Y 60	Db 1 M R M S P V F A C I A M G L A L T F A G S A S S H H Q S L A A R L T A F G V R V F Q V D V Q A S K D R N V V F S P Y 60
Qy 61 G V A S V L A M I L O L T G G E T Q O Q I Q A M G K P I D D K G M A P A I R H Y K E L M G P N K D E I S T D A I 120	Qy 61 G V A S V L A M I L O L T G G E T Q O Q I Q A M G K P I D D K G M A P A I R H Y K E L M G P N K D E I S T D A I 120
Db 61 G V A S V L A M I L O L T G G E T Q O Q I Q A M G K P I D D K G M A P A I R H Y K E L M G P N K D E I S T D A I 120	Db 61 G V A S V L A M I L O L T G G E T Q O Q I Q A M G K P I D D K G M A P A I R H Y K E L M G P N K D E I S T D A I 120
Qy 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180	Qy 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180
Db 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180	Db 121 F V Q R D I K L V Q G F M P H P F R I P R S T V Q D F S E V E R A R F I N D W K V T H T K G M I S N U L G K G A V 180
Qy 241 G H Y D I L E D P Y H G D T L S M F I A A P Y K E V P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K 300	Qy 241 G H Y D I L E D P Y H G D T L S M F I A A P Y K E V P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K Y P K 300
Db 241 G R Y D I L E D P Y H G M P F N F R I F R T I V Q V D V Q A S I T S I L D A E I S Q W K G M T R L T R L V L P K 300	Db 241 G R Y D I L E D P Y H G M P F N F R I F R T I V Q V D V Q A S I T S I L D A E I S Q W K G M T R L T R L V L P K 300
Qy 301 F S L E P D V D L K P L E N G M T M F Q Q A D F T S L D E P L H A V A Q A L O K V K I E V N E S G T V A S S 360	Qy 301 F S L E P D V D L K P L E N G M T M F Q Q A D F T S L D E P L H A V A Q A L O K V K I E V N E S G T V A S S 360

DR	Ensembl; ENSRNOG00000001414; Rattus norvegicus.	Scheetz T.E., Bonaldo M.F., Casavant T.L., Brownstein M.J., Uedin T.B., Yoshiyuki S., Carninci P., Prange C., Loguelano N.A., Peters G.J., McKernan R.D., Mulhall S.J., Raha S.S., McEwan P.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Gibbs R.A., Vidalon D.K., Muñiz D.M., Sodergren E.J., Lu X., Fahy J., Heitman B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green D.E., Dickson M.C., PANTHER; PTHR1461; Prot_inh_serpin; 1.
DR	Pfam; PF00079; Serpin; 1.	Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schein A., Schein J.B., Jones S.J.M., Marr M.A., "Generation and initial analysis of more than 15,000 full-length human serine protease inhibitor; Serpin; Signal.
DR	PROTEIN; PS00284; SERPIN; 1.	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green D.E., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schein A., Schein J.B., Jones S.J.M., Marr M.A., "Generation and initial analysis of more than 15,000 full-length human serine protease inhibitor; Serpin; Signal.
DR	Glycoprotein; Plasma; Plasminogen activation; Protease inhibitor; KW	Blakesley R.W., Touchman J.W., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schein A., Schein J.B., Jones S.J.M., Marr M.A., "Generation and initial analysis of more than 15,000 full-length human serine protease inhibitor; Serpin; Signal.
FT SIGNAL	1	By similarity.
FT CHAIN	23	Plasminogen activator inhibitor-1.
FT SITE	24	402
FT CARBOHYD	369	Reactive bond.
FT CARBOHYD	88	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	232	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	288	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	352	N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD	352	(GlcNAc. . .) (Potential).
SQ SEQUENCE	402 AA;	45010 MW;
SQ	SEQUENCE	2B639140F475BB53 CRC64;
Query Match	81-118;	Score 1680; DB 1; Length 402;
Best Local Similarity	80.8%;	Pred. No. 1.4e-126;
Matches	325;	Conservative 36; Mismatches 41; Indels 0; Gaps 0;
Qy	1	MQMSPALTCLVGLALIVPGESAVHPPSTVAHLASDFGTVFQVOVAQASKDRNVFSPY
Db	1	MQMSSALTCLTGLNLVPGKGPASPAPESHTAQCATNEGYKVFQHVQASKDRNVFSPY
Qy	61	GVASVIALMLOLTGETGTOQOQIAANGFKIDDKGMAPALRILYKELMGPKWNKDEIISTTDAI
Db	61	GVSSVIALMLQTAGTRQQIDANGFNISERGTAPALKLUSKEIMGSWNKNEISTADA
Qy	121	FVQRDLKLKVQGFMPHEFFPRFLFRSTVQVDSEVERARFLINDWVTKTHTKGMISNLGKAV
Db	121	FVQRDLKLKVQGFMPHEFFKLPRTIVQVDSEVERARFLINDWVTKHKGMSIDLAKGAV
Qy	181	DQLTRLVNVALYNGQWKRPPDSSTHRLFKSDGSTSVPMMAQTKNFTNTEFTTD
Db	181	NELTRLVNVALYNGQWKRPPLEASTHQLRHKSDGSTISVPMMAQNNKFNTTEFTTD
Qy	241	GHYDILEPLYHGDTLSMFTAAYPEKVLPSALTNLISQIASHWKGNNTRLPRLVLPK
Db	241	GHEYDILEPLYHGDTLSMFTAAYPEKVLPSALTNLISQIASHWKGNNTRLPRLVLPK
Qy	301	FSLETEVDLRLKPLENIGMTDMFROQAFDTSLSDQEPHLVQAQLQKVKEVNESCTVASS
Db	301	FSLETEVDLRLKPLENIGMTDMFROQAFDTSLSDQEPHLVQAQLQKVKEVNESCTVASS
Qy	361	STAVVSARIAAPEEIMDRPFLFYVHRNPITGTVLNGQMEP
Db	361	STAVVSARIAAPEEIMDRPFLFYVHRNPITETIFMGQMEP
RESULT 7	Q7TPB9_MOUSE	NUCLEOTIDE SEQUENCE.
ID	Q7TPB9_MOUSE	STRAIN=BS-EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
AC	Q7TPB9_	MEDLINE=2388357; PubMed=12447932; DOI=10.1073/pnas.242603899;
DT	01-OCT-2003 (TREMBLrel. 25, Created)	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
GN	Name=Serpine1; OS=Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi; Mammalia; Butharia; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
NCBI TaxID=10989;	[1]	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RP	NUCLEOTIDE SEQUENCE.	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RX	STRUETB9_MOUSE PRELIMINARY;	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	STRUETB9_MOUSE PRELIMINARY;	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	01-OCT-2003 (TREMBLrel. 25, Created)	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	01-MAR-2004 (TREMBLrel. 26, Last sequence update)	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
GN	Name=Serpine1; OS=Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi; Mammalia; Butharia; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	STRUETB9_MOUSE PRELIMINARY;	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	01-AUG-1991 (Rel. 19, Created)	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	RESULTS 8	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	STRUETB9_MOUSE STANDARD; PRT; 402 AA.	STRUETB9_MOUSE STANDARD; PRT; 402 AA.
RA	Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schulter G.D., Altuch S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	STRUETB9_MOUSE STANDARD; PRT; 402 AA.

DT	01-AUG-1991 (Rel. 19, Last sequence update)	Qy	61 GVASYTLAMQLQTGGJETQQQIAAMGPKIDDKGMHAPALRHLYKEMLGPMWKDEISSTDAI	120
DT	10-MAY-2005 (Rel. 47, Last annotation update)	Db	61 GVSSYTLAMQLMTAGKTRQIQDAMGPKNEKTAHALRQLSKELMGPWNKNESTADAI	120
DE	Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial)			
GN	Name-Serpine1; Synonyms-Wrl1; Pail; Planh1;			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii; Muroidea; Muridae; Murinae; Mus.			
OC	NCBI_Taxid=10090;	Qy	121 FVQRDLKLYQGFMPFFRLFRSTYQDFSEVERARFTINDWYKTHKOMISNLIGKGAV	180
RP	NUCLEOTIDE SEQUENCE RXNDBLNE=90158593; PubMed=2406566;	Db	121 FVQRDLKLYQGFMPFFRLFRSTYQDFSEVERARFTINDWYKTHKOMISNLIGKGAV	180
RA	Prendergast G.C.; Diamond L.E.; Dahl D.; Cole M.D.; RT 1.";	Qy	181 DQLFPLVLYNALYFGQWKTPEPDSSTHERLFHKSDGSTVSPMAQTMKFNYTEFTPD	240
RT	"The c-myc-regulated gene mri encodes plasminogen activator inhibitor 1."	Db	181 DELTALVLYNALYFGQWKTPEFASHTORLFHKSDGSTVSPMAQSNSKPNYTEFTPD	240
RL	Mol. Cell. Biol. 10:1265-1269 (1990).	Qy	241 GHYYDLEPLYHGDSLMSMFTAAPKEVPLSALNILSAQLISHWKGMNTRLPPLVLPK	300
RN	[2]	Db	241 GLEYDVVELPYQDRDLSMFTAAPKEVPLSALNILDAELIRQMGKGMNTRLPPLVLPK	300
RP	PROTEIN SEQUENCE OF 23-29.	Qy	301 FSLETEVDLRLKPYLENLGMGTMDFRQFQADFPLSLSDQEPLVIAQALQKVKEVNESGVASS	360
RX	PubMed=7523120;	Db	301 FSLETEVDLRLKPYLENLGMGTMDFRQFQADFPLSLSDQEPLVIAQALQKVKEVNESGVASS	360
RA	Lijnen H.R.; van Hoef B.; Beelen V.; Collen D.; RT "Characterization of the murine plasma fibrinolytic system.";	Qy	361 STAVIVSARNAAPEEITIMDREPFLFVTRHNPTGTIVLFGQWMEP	402
RL	Eur. J. Biochem. 224:863-871 (1994).	Db	361 STAVIVSARNAAPEEITIMDREPFLFVTRHNPTGTIVLFGQWMEP	402
CC	-I- FUNCTION: This inhibitor acts as "bait" for tissue plasminogen activator, urokinase, and protein C. Its rapid interaction with tPA may function as a major control point in the regulation of fibrinolysis.			
CC	-I- SUBUNIT: Interacts with tPA. Binds LRPIB; binding is followed by internalization and degradation (By similarity).			
CC	-I- INTERACTION: Q5248-Descri; NbExp=1; IntAct=EBI-490889;			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: Belongs to the serpin family.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.			
CC	DR EMBL; M39660; AAA39887.1; - ; mRNA.			
DR	DR PIR; A34761; A34761.			
DR	DR HSSP; P05122; 1DAM.			
DR	DR P22777; 29-402.			
DR	DR IntAct; P22777; - .			
DR	DR EnsembL; ENSMUSG00000037411; Mus musculus.			
DR	DR MGI; MGI_97608; Serpine1.			
DR	DR GO; GO_0005615; C:extracellular space; TAS.			
DR	DR GO; GO_0005515; F:protein binding; IPI.			
DR	DR GO_0045765; F:regulation of angiogenesis; IDA.			
DR	DR InterPro; IPR000215; Prot_inh_serpin.			
DR	DR PANTHEA; PTHR1.141; Prot_inh_serpin.			
DR	DR Pfam; PF00079; Serpin_1.			
DR	DR PROSITE; PS00284; SERPIN_1.			
KW	Direc protein sequencing; Glycoprotein; Plasma; Serine protease inhibitor; Serpin activation; Protease inhibitor; Serine protease inhibitor;			
KW	Plasminogen activation; Probable.			
KW	Serpin; Signal; 22			
FT	FT SIGNAL 1	Query Match	60.6%; Score 1256;	DB 2; Length 280;
FT	FT CHAIN 23	Best Local Similarity	86.4%; Pred. No. 1.2e-92;	
FT	FT SITE 369	Matches	242; Conservative 17; Mismatches 21; Indels 0; Gaps 0;	
FT	FT CARBOHYD 232	Qy	107 GPWNKDEISTDAIFQDLDLKVQDFSEVERARFTINDWYKTH 166	
FT	FT CARBOHYD 288	Db	1 GPWNKDEISTDAIFQDLDLKVQDFSEVERARFTINDWYKTH 60	
FT	FT CARBOHYD 352			
FT	FT CONFLICT 23			
SEQ	SEQUENCE 402 AA: 45170 MW; 765FFI659CT0F68C CRC64;			
FT	FT SIGNAL 1	Qy	167 TKGMISNLGKGMGAVDOLTRLVLYNALYFGQWKTPEPDSSTHRLPHKSDGSTVSPYMA	226
FT	FT CHAIN 23	Db	61 TKGMISNLGKGMGAVDOLTRLVLYNALYFGQWKTPEPDSSTHRLPHKSDGSTVSPYMA	120
FT	FT SITE 370			
FT	FT CARBOHYD 232			
FT	FT CARBOHYD 288			
FT	FT N-linked (GLCNAC. . .) (Potential).			
FT	FT N-linked (GLCNAC. . .) (Potential).			
FT	FT N-linked (GLCNAC. . .) (Potential).			
FT	FT T > M (In Ref. 2).			
SEQ	SEQUENCE 402 AA: 45170 MW; 765FFI659CT0F68C CRC64;			
FT	FT SIGNAL 1	Qy	227 QTNKFNTEFTPDGHYDILELPYHGDTLSMFIAAPYEKVPYASQDRNRYFSPY	60
FT	FT SIGNAL 1	Db	1 MQNSPALTCLVLGHALYVGEGSAVHHPYSVYAHLSDFGRVYEQQAQSKDRNRYFSPY	60
FT	FT SIGNAL 1			

Qy	287	GNNTRLPLPILYLPKSLETEVDRKPLENLUGMTDMFQADFTSLSDQEPHVAQALQK	346	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Db	181	RSMTRVRLVLPKESLEVDLRLRPLENLGMDTDFRNPQADFTSINQELLHVSQALQK	240	Xenopoda; Xenopus; Xenopus; Xenopus; Xenopus [1]
Qy	347	VKIEVNESTGVASSSTAVIYSARMAPEEIMDRPLFLVVR	386	OC OC_XENLA PRELIMINARY; RN [1]
Db	241	VKIEVNESTGVASSSTGVASARMAPEEIMDRPLFLVVR	280	OC_XENLA PRELIMINARY; RN [1]
RESULT 10				
077772	RABBIT PRELIMINARY;	PRT;	182 AA.	OC_XENLA PRELIMINARY; RN [1]
AC	077772;	O77772;	Created)	OC_XENLA PRELIMINARY; RN [1]
DT	01-NOV-1998	(TREMBLrel. 08,	Last sequence update)	OC_XENLA PRELIMINARY; RN [1]
DT	01-NOV-1998	(TREMBLrel. 08,	Last annotation update)	OC_XENLA PRELIMINARY; RN [1]
DB	Putative plasminogen activator inhibitor-1 (Fragment).			OC_XENLA PRELIMINARY; RN [1]
OS	Oryctolagulus cuniculus (Rabbit).			OC_XENLA PRELIMINARY; RN [1]
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC_XENLA PRELIMINARY; RN [1]
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;			OC_XENLA PRELIMINARY; RN [1]
OC	Oryctolagulus.			OC_XENLA PRELIMINARY; RN [1]
NCBI_TaxID	9986;			OC_XENLA PRELIMINARY; RN [1]
OX				OC_XENLA PRELIMINARY; RN [1]
NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Lung;			RC TISSUE=Spleen.
RA	Yin J., Ideil S.,			RA TISSUE=Spleen.
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			RA TISSUE=Spleen.
CC	-!- SIMILARITY: Belongs to the serpin family.			RA TISSUE=Spleen.
DR	EMBL; AF07325; EAC2632.1; -; mRNA.			RA TISSUE=Spleen.
DR	HSSP; P05121; I1J55.			RA TISSUE=Spleen.
SMR;	077772; 1-182.			RA TISSUE=Spleen.
DR	GO; GO:0000867; F:serine-type endopeptidase inhibitor activity; IEA.			RA TISSUE=Spleen.
DR	InterPro; IPR00215; Prot_inh_serpin.			RA TISSUE=Spleen.
PFAM;	PF00079; Serpin; 1.			RA TISSUE=Spleen.
SMART;	SM00093; SERPIN; 1.			RA TISSUE=Spleen.
KW	Serpin.			RA TISSUE=Spleen.
FT	NON_TER 1	1		RA TISSUE=Spleen.
FT	NON_TER 182	182		RA TISSUE=Spleen.
SQ	SEQUENCE 182 AA;	182 AA;	Score 863, DB 2; Length 182;	RA TISSUE=Spleen.
Query Match	41.7%			RA TISSUE=Spleen.
Best Local Similarity	88.5%			RA TISSUE=Spleen.
Matches 161;	Conservative 13; Nismatches 8; Indels 0; Gaps 0;			RA TISSUE=Spleen.
Qy	101 LYKELMGPWNKDEISTDAFVQDIIKLVQGFMPIFFRLFRSTVQDVDFSEVEARFIN	160	Qy 101 LYKELMGPWNKDEISTDAFVQDIIKLVQGFMPIFFRLFRSTVQDVDFSEVEARFIN 160	Qy 101 LYKELMGPWNKDEISTDAFVQDIIKLVQGFMPIFFRLFRSTVQDVDFSEVEARFIN 160
Db	1 LSKELMGPWNKDEISTDAFVQDIIKLVQGFMPIFFRLFRSTVQDVDFSEVEARFIN 60			Db 1 LSKELMGPWNKDEISTDAFVQDIIKLVQGFMPIFFRLFRSTVQDVDFSEVEARFIN 60
Qy	161 DWVKTHTKGMTISNLIGKGAVDQLTRIVLNALYNGQKTPFPDSSTTHRLFKSDGSTV	220	Qy 161 DWVKTHTKGMTISNLIGKGAVDQLTRIVLNALYNGQKTPFPDSSTTHRLFKSDGSTV 220	Qy 161 DWVKTHTKGMTISNLIGKGAVDQLTRIVLNALYNGQKTPFPDSSTTHRLFKSDGSTV 220
Db	61 DWVKTHTKGMTISNLIGKGAVDQLTRIVLNALYNGQKTPFPDSSTTHRLFKSDGSTV 120			Db 61 DWVKTHTKGMTISNLIGKGAVDQLTRIVLNALYNGQKTPFPDSSTTHRLFKSDGSTV 120
Qy	221 SVPMQAQTNKFNTEFTPDGHYYDILELPYHGDTLSMFTAAPYKEPVIPSLATNLISAQ	280	Qy 221 SVPMQAQTNKFNTEFTPDGHYYDILELPYHGDTLSMFTAAPYKEPVIPSLATNLISAQ 280	Qy 221 SVPMQAQTNKFNTEFTPDGHYYDILELPYHGDTLSMFTAAPYKEPVIPSLATNLISAQ 280
Db	121 SVPMQAQTNKFNTEFTPDGHYYDILELPYHGDTLSMFTAAPYKEPVIPSLATNLISAK	180	Db 121 SVPMQAQTNKFNTEFTPDGHYYDILELPYHGDTLSMFTAAPYKEPVIPSLATNLISAK 180	Db 121 SVPMQAQTNKFNTEFTPDGHYYDILELPYHGDTLSMFTAAPYKEPVIPSLATNLISAK 180
Qy	281 LI 282			Qy 281 LI 282
Db	181 LI 182			Db 181 LI 182
RESULT 11				
Q6DD81	XENLA PRELIMINARY;	PRT;	395 AA.	Q6DD81-XENLA PRELIMINARY; AC Q6DD81;
AC	Q6DD81;			AC Q6DD81;
DT	25-OCT-2004 (TREMBLrel. 28, Created)			DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DB	Serpine2-prov protein.			DB Serpine2-prov protein.
GN	Xenopus laevis (African clawed frog).			GN Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db	261 STPLSAIIPIHISTKTLQSW---MTMSPKRVOLILPKFSEADELKEPRLRNGLITEMPPDV	317	CC removed.	
Qy	326 FQADFTLSQDOPFLVLAQLQKVKEEVNEFGTVASSSTAVTSSARMAPSEIIMDRPFLV	384	CC EMBL; X70296; CAA9777_1; - ; mRNA. DR EMBL; BC010675; AAH10675_1; - ; mRNA. DR EMBL; X70946; CAA0285_1; - ; Genomic_DNA.	
Db	318 SKANFAKISRSSESLEHVSHLQKAKIEVNEFGTKASSGATTAVALIARSSPRWFTVDRPFLF	377	DR PIR; I48717; I48717. DR HSSP; Pos121; IDB2. DR Ensembl; ENSMUSG0000002649; Mus musculus. DR MGI; MGI:1101780; Serpin2. DR GO; GO:0005615; C extracellular space; TAS.	
Qy	385 VRHNPTGTIVFMGQYMEP	402	DR InterPro; IPR000215; Prot_inh_serpin. DR PANTHER; PTHR11461; Prot_Inh_serpin; 1. DR Pfam; PF00079; Serpin; 1. DR SMART; SM00093; SERPIN; 1. DR PROSITE; PS00284; SERPIN; 1.	
Db	378 IRHNPTGAVALFTGQINRP	395	KW Developmental_protein; Differentiation; Glycoprotein; Heparin-blinding; KW Neurogenesis; Protease inhibitor; Serine protease inhibitor; Serpin; KW Signal.	
RESULT 12			FT SIGNAL 1 19 By similarity. Glia derived nexin. Reactive bond (By similarity). FT CHAIN 20 397 N-linked (GlcNAc, . .) (Potential). FT SITE 364 365 I -> V (In Ref. 2). FT CARBHYD 159 159 CONFLICT 313 313 44207 MW; B8EBBAE3CA89904A5 CRC64; SQ SEQUENCE 397 AA; 38 5%; Score 796.5; DB 1; Length 397;	
GDN_MOUSE		RN [1]	Query Match 38 Local Similarity 43.0%; Pred. No. 1.9e-55; Gaps 2; Matches 159; Conservative 74; Mismatches 134; Indels 3; Gaps 2;	
ID	GDN_MOUSE STANDARD;	PRT;	397 AA.	
AC	Q211T7;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-FEB-1996 (Rel. 31, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DB	Glia derived nexin precursor (GDN) (Protease nexin 1) (Serine protease-inhibitor-4).			
GN	Name=terpine2; Synonyms=517, Pn1, Spi4;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Benthida; Euarchontoglires; Giresi; Rodentia; Sciurognathii;			
OC	Muroidea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	NUCLEOTIDE SEQUENCE.			
RA	Belin D.; Submitted (SEP-1994) to the EMBL/GenBank/DDJB databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MENA].			
RP	Medline:12477932; DOI:10.1073/pnas.242603899;			
RP	ME22388257; PubMed:12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		Qy 34 LASDFGVRFQVQAGAQSKDRNRYVFSPPGYASVSLAMQLQTGGETQQIQAAMGFIDDKG 93 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.P., Casarav T.J., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.A., McEvaw P.J., McKernan K.J., Malek J.A., Gutarate P.H., RA Richards S., Worley K.C., Garcia A.M., Gay J.J., Hulyk S.W., RA Villacon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketten M., Madan A., Rodriguez S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.; RT Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.".	
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	NUCLEOTIDE SEQUENCE OF 1-366.			
RC	STRAIN-BALB/c;			
RX	Medline:93259128; PubMed:891179;		RESULT 13 Q543R5_MOUSE PRELIMINARY; PRT; 397 AA.	
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,		ID Q543R5; 13-SEP-2005 (TREMBLref). 31, Created	
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,		DT 13-SEP-2005 (TREMBLref). 31, Last sequence update	
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."		DT 13-SEP-2005 (TREMBLref). 31, Last annotation update	
RX	EMBO J. 12:1871-898 (1993)		DE 16-days embryo head cDNA, RIKEN full-length enriched library, clone:C13010H12 product:serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, full insert sequence (12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130035K01 product:serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2, full insert sequence (Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library,	
CC	FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting thrombin. Binds heparin.		This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not	
CC	SUBCELLULAR LOCATION: Extracellular.			
CC	- TISSUE SPECIFICITY: Most abundant in seminal vesicles.			
CC	- SIMILARITY: Belongs to the serpin family.			
CC	RT This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not			
RN	NUCLEOTIDE SEQUENCE OF 1-366.			
RC	STRAIN-BALB/c;			
RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
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RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
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RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
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RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
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RC	STRAIN-BALB/c;			
RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
RX	EMBO J. 12:1871-898 (1993)			
CC	FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting thrombin. Binds heparin.			
CC	SUBCELLULAR LOCATION: Extracellular.			
CC	- TISSUE SPECIFICITY: Most abundant in seminal vesicles.			
CC	- SIMILARITY: Belongs to the serpin family.			
CC	RT This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not			
RN	NUCLEOTIDE SEQUENCE OF 1-366.			
RC	STRAIN-BALB/c;			
RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
RX	EMBO J. 12:1871-898 (1993)			
CC	FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting thrombin. Binds heparin.			
CC	SUBCELLULAR LOCATION: Extracellular.			
CC	- TISSUE SPECIFICITY: Most abundant in seminal vesicles.			
CC	- SIMILARITY: Belongs to the serpin family.			
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RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
RX	EMBO J. 12:1871-898 (1993)			
CC	FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting thrombin. Binds heparin.			
CC	SUBCELLULAR LOCATION: Extracellular.			
CC	- TISSUE SPECIFICITY: Most abundant in seminal vesicles.			
CC	- SIMILARITY: Belongs to the serpin family.			
CC	RT This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not			
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RC	STRAIN-BALB/c;			
RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
RX	EMBO J. 12:1871-898 (1993)			
CC	FUNCTION: Serine protease inhibitor with activity toward thrombin, trypsin, and urokinase. Promotes neurite extension by inhibiting thrombin. Binds heparin.			
CC	SUBCELLULAR LOCATION: Extracellular.			
CC	- TISSUE SPECIFICITY: Most abundant in seminal vesicles.			
CC	- SIMILARITY: Belongs to the serpin family.			
CC	RT This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not			
RN	NUCLEOTIDE SEQUENCE OF 1-366.			
RC	STRAIN-BALB/c;			
RX	Medline:93259128; PubMed:891179;			
RX	Vassalli J.-D., Huarte J., Bosco D., Sappino A.P., Sappino N.,			
RX	Velardi A., Wohlwend A., Bruno H., Monard D., Belin D.,			
RX	"protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle."			
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RX	Medline:93259128; PubMed:891179;			
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RC	STRAIN-BALB/c;			
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CC	- TISSUE SPECIFICITY: Most abundant in seminal vesicles.			
CC	- SIMILARITY: Belongs to the serpin family.			
CC	RT This Swiss-Prot entry is copyright. It is			

Qy	273	LTNLSQLISHWKGNTRPLBLVLPKFSLETVDLRKPLENGLMTDMQFRQFADFTSL	3327
Db	268	IIPHITKTIDSWNATMVKRMQLVLPKETAVQTDLKREPLKAIGITMEPESSANFIKI	3277
Qy	333	SDQEPLHVAQALQKVIEVNESGTVASSSTAVIISARMAPEEIIIMDRPFLFVVRHNPTGT	3934
Db	328	TRSESLHVSHILQAKIEVSEDGTASAATTAILIARSSPPWFIVDRPFLFSIRHNPTGA	3877
Qy	393	VLFMGQVMEP	402
Db	388	ILFLGQVNKP	397
RESULT 14			
Qy	273	RESULT 14 Q4FJU1_MOUSE Q4FJU1_MOUSE PRELIMINARY;	PRT; 397 AA.
Db	AC	Q4FJU1_	
	DT	13-SEP-2005 (TREMBLE). 31. Created)	
	DT	13-SEP-2005 (TREMBLE). 31. Last sequence update)	
	DT	13-SEP-2005 (TREMBLE). 31. Last annotation update)	
Qy	333	Serpine2 protein.	
Db	GN	Name-Serpine2;	
Qy	333	Mus musculus (Mouse).	
Db	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.	
Qy	333	NCBI_TaxID=10090;	
Db	RN	[1]	
NUCLEOTIDE SEQUENCE.			
Qy	333	Ebert L., Muenchmann E., Schatten R., Henze S., Bohn E., Mollenhauer J., Wiemann S., Schick M., Korn B.;	
Db	94	"Cloning of mouse full open reading frames in Gateway(R) system entry vector (pDON201)." Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.	
Qy	333	EMBL: CT010311; CAJU8519.1; -; mRNA.	
Db	DR	SEQUENCE 397 AA; 44193 MW; F775413CBE36863 CRC64;	
Qy	34	Query Match 38.5%; Score 796.5; DB 2; Length 397; Best Local Similarity 43.0%; Mismatches 134; Indels 3; Gaps 2; Matches 159; Conservative 74; MisMatches 134;	
Db	93	IASDFCVRQQAQSQRDNVYFSPYGVASVLAQMLQLTTGCTQQQIQAAAGFKIDDKG	
Qy	30	LGNTGQVNPQIKSRPHENVVSPHGTASILGMQLGADGKTKQLSTMVRNNN-G	
Db	87	87	
Qy	94	MAPALRHLYKELMGPWQKDLSITDAIFQVDRKLVQGMFMHPFPRFLFRSTVQVDESEVE	
Db	15	15.000000000000001	
Qy	88	VGRVLRKINKAIVSKRNKDITYVANAVFLERNFGKEVFPFAVRKVQYFQCEQNQNFDPA	
Db	14	14.000000000000001	
Qy	154	PARFLINDWVKTTHKGMISNLGKGAVD-QLTRVLVNLAYFGNKQWTFFPDSTSRRFLF	
Db	21	21.000000000000001	
Qy	148	SASESINFNWKNTRGNIDLSPNLDGAITRLVNAVTFKGLMKSRFPESTEYKRTF	
Db	20	20.000000000000001	
Qy	213	HKSDFGTSVPMMAQCNKNTYTFPDGHYYDILFLPYHGDTLSMFLIAAPYKEVPLSA	
Db	27	27.000000000000001	
Qy	208	VAGDGKSYQVPMLAQSVERSGSTPENGWNYNFIELPYHGBISMIALPTESSTPLSA	
Db	26	26.000000000000001	
Qy	273	LTNLSQLISHWKGNTRPLBLVLPKFSLETVDLRKPLENGLMTDMQFQQAQFTSL	
Db	33	33.000000000000001	
Qy	268	IIPHITKTIDSWNATMVKRMQLVLPKETAVQTDLKREPLKAIGITMEPESSANFIKI	
Db	32	32.000000000000001	
Qy	333	SDQEPLHVAQALQKVIEVNESGTVASSSTAVIISARMAPEEIIIMDRPFLFVVRHNPTGT	
Db	39	39.000000000000001	
Qy	328	TRSESLHVSHILQAKIEVSEDGTASAATTAILIARSSPPWFIVDRPFLFSIRHNPTGA	
Db	38	38.000000000000001	
RESULT 15			
GDN_RAT	388	VLFMGQVMEP	402
ID	388	ILFLGQVNKP	397
Qy	393	RESULT 15 STANDARD;	PRT; 397 AA.
Db	388	STANDARD;	PRT; 397 AA.

```

Db    88  vGKVKKINKAIAVSKKNDIVTVANAVFVRNGFKVEVPAARNKEVFQCEVQSUNFQDDA 147
Qy   154  RARFLINDWYTKHTKGMINSLGKGAVDQ-LTRLVNVNLYENGOWKTPEPDSSSTHRLRF 212
Db    148  SACDAINFWYKNETRGMIDNLSPNLJDSALTKLVLVNAVYFKGLWKSFQPEENTKCF 207
Qy   213  HKSDGSTVSYPMMAGTNKNEYTEFTTPDGHHYDILELPYHGTLSMFIAPYEKEVPLSA 272
Qy   213  HKSDGSTVSYPMMAGTNKNEYTEFTTPDGHHYDILELPYHGTLSMFIAPYEKEVPLSA 272
Db    208  VAGDGKSYQYBMLAQLSVFRSGSTKTPNGIWNFTELPYGEISSMILALPTESTPLSA 267
Qy   273  LTNLISAQLISHWKGNMTRPLRLVLPKFSLTEVDLRKELENUGMTDNFRQFOADFTSL 332
Db    268  LIPHISTKTINSWMNTMVKRMQLVLPKFALAAQDLKBP1KALGITEFEPSKANFAKI 327
Qy   333  SDQEPLRVQAQLQKVYIEENESGTVASSSTAVIVSARMAPAEIIIMDRPFLFVVRHNPTGT 392
Db    328  TRSESHVSHLQKAKIEVEDGTXAATVTTAILARSSPPWFIVDRPFLFCIRHNPTGA 387
Qy   393  VLFMGQYMEP 402
Db    388  ILFLGQYNKP 397

```

Search completed: December 13, 2005, 09:08:39
 Job time : 235 secs

Gendcore version 5.1.6
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Om protein - protein search, using bw model.

Run on: December 13, 2005, 15:46:54 ; Search time 189 seconds
 (without alignment(s))
 934.552 Million cell updates/sec

Title: US-10-506-406-2

Perfect score: 2071

Sequence: 1 NQMSPALTCVLGLALVFGE.....FVVRHNPTGTVLFMQVMEP 402

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:
 1: GeneseqP1980s:
 2: GeneseqP1990s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003s:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 9: GeneseqP2005s:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	402	2 AAV31587	Aaw31587 Human pla
2	2071	100.0	402	4 AAU04913	Aau04913 Human pla
3	2071	100.0	402	4 AAB90794	Aab90794 Human she
4	2071	100.0	402	5 ABP65137	Abp65137 Hypoxia-r
5	2071	100.0	402	5 AAE14271	Aae14271 Plasminog
6	2071	100.0	402	5 ABP68605	Abp68605 Human pan
7	2071	100.0	402	6 AAE37331	Aae37331 Human pla
8	2071	100.0	402	6 ABR82199	Abr82199 Human pla
9	2071	100.0	402	7 ABR63123	Ab63123 Human pla
10	2071	100.0	402	7 ADP28929	Adp28929 Human pla
11	2071	100.0	402	7 ADP28771	Adp28771 Human pla
12	2071	100.0	402	7 ABW02690	Abw02690 Human pla
13	2071	100.0	402	7 ADN95544	Adn95544 Human BBC
14	2071	100.0	402	8 ADT75605	Adt75605 Marker ge
15	2071	100.0	402	8 ADL35812	Adl35812 Human pla
16	2071	100.0	402	8 ADD05046	Add05046 Human pla
17	2071	100.0	402	8 ABM80915	Abm80915 Tumour-as
18	2071	100.0	402	8 ADP3374	Adp3374 PRO polyp
19	2071	100.0	402	8 ADQ39257	Adq39257 Human myo
20	2071	100.0	402	8 ADQ39256	Adq39256 Human myo
21	2071	100.0	402	9 ADV70216	Adv70216 Tumor-as
22	2071	100.0	402	9 AEAB1039	Aeb1039 Human pla
23	2071	100.0	402	9 AEB29725	Aeb29725 Human Ser
24	2067	99.8	402	2 AAR07986	Aar07986 Plasminog

ALIGNMENTS

RESULT 1	
ID	AAW31587 standard; protein; 402 AA.
XX	
AC	AAW31587;
XX	
DT	14-APR-1998 (first entry)
XX	Human plasminogen activator inhibitor type 1.
DE	
XX	
KW	Plasminogen activator inhibitor type 1; PAI-1; human; elastase inhibitor;
KW	vitronectin; cell attachment; cell migration; cell proliferation; acute lung inflammation;
KW	empysema; adult respiratory distress syndrome; cystic fibrosis; atopic dermatitis;
KW	alpha 1-antitrypsin deficiency; pancreatic; periodontal disease; arthritis; HIV; atherosclerosis;
KW	pancreatitis; neointima; fibrosis; wound healing; tumour; metastasis;
KW	psoriasis; thrombosis; angiogenesis; therapy.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	1..23
Peptide	/label= Sig_peptide
PT	24 ..402
Protein	/label= Mat_Protein
PT	/note= "Claim 3"
Misc-difference	173 /note= "preferred substitution site for protein
FT	stabilisation"
FT	Misc-difference 177 /note= "preferred substitution site for protein
FT	stabilisation"
Misc-difference	342 /note= "preferred substitution site for protein
FT	stabilisation"
FT	354 ..375 /note= "reactive centre loop region"
Region	
FT	
Misc-difference	366 /label= P1
FT	/note= "preferred substitution site to provide elastase
FT	inhibitor mutant"
FT	Misc-difference 369 /label= P1
FT	/note= "preferred substitution site to provide elastase
FT	inhibitor mutant"
FT	Misc-difference 377 /note= "preferred substitution site for protein

PT XX Substitution

PN WO939028-A1.

XX 23-OCT-1997.

PD 11-APR-1997; 97WO-US006071.

PF 12-APR-1996; 96US-0015299P.

PR (AMNIA-) AMERICAN NAT RED CROSS.

XX Lawrence DA, Stefansson SP;

PI DR WPI; 1997-526399/48.

DR N-PsDB; AAT9703.

XX Plasminogen activator-inhibitor type I mutant inhibits elastase - or has high affinity for vitronectin, for therapeutic inhibition of elastase or vitronectin-mediated cell attachment, migration etc.

XX Claim 3; Fig 4A; 14pp; English.

CC This polypeptide sequence comprises wild-type human plasminogen activator inhibitor type (PAI-1). Novel mutants (see AAW26710-25) of the PAI-1 mature protein are claimed that inhibit elastase or other elastase-like proteases, or are inhibitors of vitronectin-dependent cell migration. The mutants are obtained by site-directed mutagenesis of the PAI-1 DNA sequence (see AAT97303) and expression in host cells, and have a range of therapeutic uses. Preferred mutants have amino acid substitutions in the reactive centre loop region (especially at position 343 and/or 346 of the mature protein), and may have additional stabilising amino acid substitutions at 1-4 of residues 150, 154, 319 and 354, and 1-5 of residues 333, 335, 371, 372 and 91.

SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 2; Length 402; Best Local Similarity 100.0%; Pred. No 4.4e-190; Mismatches 0; Indels 0; Gaps 0; Matches 400; Conservative 0; Gaps 0;

Qy 1 MQMSPALTCLVGLALVFGEGSAVHPPSYVAHLASDEGVRFQVQAQASKDRNVVFSSY 60

Db 1 MQMSPALTCLVGLALVFGEGSAVHPPSYVAHLASDEGVRFQVQAQASKDRNVVFSSY 60

Qy 61 GVASVTLMLQLTTGGEBTQQIQAANGFKIDDKGMPKDEISETDDAI 120

Db 61 GVASVTLMLQLTTGGEBTQQIQAANGFKIDDKGMPKDEISETDDAI 120

Qy 121 FVQRDLKLVQGFMPIFFRLFRSTYKVQDFSEVERAFINDWVKTHTKGMISNLGKAV 180

Db 121 FVQRDLKLVQGFMPIFFRLFRSTYKVQDFSEVERAFINDWVKTHTKGMISNLGKAV 180

Qy 181 DQLTRLVLYNALYFNGQWKTTPFDPDSSTHRLFKSDGSTVSVPMMAQTNKTFNTBFITPD 240

Db 181 DQLTRLVLYNALYFNGQWKTTPFDPDSSTHRLFKSDGSTVSVPMMAQTNKTFNTBFITPD 240

Qy 241 GHYDILELPYHGDTLSMFTAAPIPKVEPIPSALTNLSQLISHWKGNTRLPRLLVFK 300

Db 241 GHYDILELPYHGDTLSMFTAAPIPKVEPIPSALTNLSQLISHWKGNTRLPRLLVFK 300

Qy 301 FSLEYEVDLRKPLENLGMDFQADFTSLSDOEPLIVAOQLKVKIEVNESGTVAASS 360

Db 301 FSLEYEVDLRKPLENLGMDFQADFTSLSDOEPLIVAOQLKVKIEVNESGTVAASS 360

Qy 361 STAVIVSARMAPAEETIMDRPFLFVYRNPPTGTVLFMGQMEP 402

Db 361 STAVIVSARMAPAEETIMDRPFLFVYRNPPTGTVLFMGQMEP 402

XX AC AAU04913;

XX DT 26-SEP-2001 (first entry)

XX Human Plasminogen activator inhibitor-1, PAI-1.

KW Human; Plasminogen activator inhibitor-1; PAI-1; serpin; immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome; ARDS; HIV infection; Human immunodeficiency virus; prostate cancer; TNF mediated inflammation; benign prostatic hypertrophy.

XX OS Homo sapiens.

XX FH Key Peptide

XX FT Peptide /label= Signal_peptide /notes= "Alternative signal peptide"

XX FT Peptide /label= Signal_peptide /notes= "Both mature forms are detectable in vivo"

XX FT Protein /label= Mature_PAI-1 #1 /notes= "Alternative signal peptide"

XX FT Protein /label= Mature_PAI-1 #2 /notes= "Both mature forms are detectable in vivo"

XX FT Region /label= Reactive_centre_loop /notes= "Reactive_centre_loop"

XX PN WO200138560-A2.

XX PD 31-MAY-2001.

XX PF 22-NOV-2000; 2000WO-US032315.

XX PR 22-NOV-1999; 99US-0167553P.

XX PA (ANNA-) AMERICAN NAT RED CROSS.

XX PI Lawrence DA, Day D;

XX DR WPI; 2001-441438/47.

XX DR N-PsDB; AAS03460.

XX PT Detecting a functionally active form of an enzyme in a biological sample comprising contacting an enzyme inhibitor immobilized on a solid substrate.

XX PS Disclosure; Fig 5; 69bp; English.

CC The sequence represents human plasminogen activator inhibitor-1, PAI-1, a serine protease inhibitor or serpin. The protein is used to demonstrate the method of the invention which comprises detecting a functionally active form of an enzyme in a biological sample by contacting an enzyme inhibitor on a solid substrate with the biological sample and measuring the binding of the enzyme inhibitor to the active form of the enzyme by a detectable label, where the enzyme inhibitor specifically forms a covalent bond or binds with a dissociation constant of 1×10^{-9} M or less with the active form of the enzyme. The present invention provides a sensitive method for the detection of a functionally active form of an enzyme in a biological sample. Human PAI-1 can be used to detect a number of enzymes including tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil elastase, pancreatic elastase, trypsin, chymotrypsin, cathepsin G and prostate specific antigen and as such can be used in methods to diagnose diseases such as cystic fibrosis, acute respiratory distress syndrome (ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and benign prostatic hypertrophy.

XX SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 4; Length 402; Best Local Similarity 100.0%; Pred. No. 4.4e-190; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
AAU04913 standard; protein; 402 AA.
ID AAU04913

types under different conditions and identifying a differentially regulated gene.

Claim 35; Page 338; 538pp; English.

The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome or a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV778173-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

Sequence 402 AA;	Query Match	100.0%	Score 2071;	DR 5;	Length 402;
Best Local Similarity	100.0%		Pred. No 4_4e-190;		
Matches 402;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

1 M0NSPALTCLVGLALVFGEGSAVHPPSPYVAHLASDFGVRFQOVAQASKDNRNVTFSPY 60
 | | | | | | | | | | | | | | | | | |
 | | | | | | | | | | | | | | | | |
 1 M0NSPALTCLVGLALVFGEGSAVHPPSPYVAHLASDFGVRFQOVAQASKDNRNVTFSPY 60

61 GVASVLAMQLRTGGTQQIQAANGFKIDDKGMAPRLHYKELMGPWNKDE1ISTDAI 120
61 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GVASVLAMQLRTGGTQQIQAANGFKIDDKGMAPRLHYKELMGPWNKDE1ISTDAI 120

121 FVORDKLVQGFMPHFRLFRSTYKQDFSEVERARFLINDMWKTHTKGMISNLJGKAV 180
121 FVORDKLVQGFMPHFRLFRSTYKQDFSEVERARFLINDMWKTHTKGMISNLJGKAV 180

241 GHYYDILELPYKGDTLSMFTAAPYEKEVPLSALTNLISAQLISHWKGNTMLPRLVLPK 300
241 GHYYDILELPYKGDTLSMFTAAPYEKEVPLSALTNLISAQLISHWKGNTMLPRLVLPK 300

301 FSLTEVDLIRKPLNLGMGTMDFRQQAQDFTSLSDQEPFLHYAQALORYKIEVNESSGVASS 360
301 FSLTEVDLIRKPLNLGMGTMDFRQQAQDFTSLSDQEPFLHYAQALORYKIEVNESSGVASS 360

361 STAVIVSARMAPPERTIMDRPFLFVVRHNPPTGTVLPGQYMEP 402
361 STAVIVSARMAPPERTIMDRPFLFVVRHNPPTGTVLPGQYMEP 402

SUIT 5
CIVIL NO. 42-10004

E142/1
AAE14271 starved; protein; 402 AA.
AAE14271;
AAE14271;

07-AUG-2003 (revised)
07-MAR-2002 (first entry)

systemic lupus erythematosus; **ovulation;** **cystostatic;** **gene therapy;** **prostatic involution;** **osteonecrosis;** **breast cancer;** **pregnancy.**

unidentified.

pathological disorders.

The invention relates to nucleic acids encoding pancreas-derived plasminogen activator inhibitor (PAI) protein. Plasminogen activator inhibitor (PAI) 1 and 2 are involved in many physiological and pathological processes, including normal pregnancy, preeclampsia, intrauterine growth retardation, wound healing, tumour cell invasion and metastasis, inflammation and arthritis, inflammatory bowel disease.

appendicitis, complications from systemic lupus erythematosus, ovulation and prostatic involution and osteonecrosis. PAPAI DNA is used to treat physiological and pathological conditions including breast cancer and to detect pathological disorders. PAPAI DNA is used in gene therapy. The present amino acid sequence is a PAI protein. (updated on 07-Aug-2003 to correct OS field.)

卷之三

Sequence 402 AA;
Query Match 100.0%; Score 2071; DB 5;
Best Local Similarity 100.0%; Pred. No. 4_4e-190; Length 402;

1 MQMSSALTIVLGLALVFGEGSAVTHPPSYVAHLASDFGYRVFQQVAQASKDNRVFSPY 60
61 GVASYLAMIQLTTGGTQQOIQAMGFK1DDKGKMAPALRHLYKSLMGPKNKDEISTTDAI 120

61	GVASVLMQLTGGTETQQIQAANGFKDDKGNAPALRHLYKELMGPNKDEISTTDAI	120
121	FVQRDLKLIVQGFMPHFFRLERSTYKVQDSEVERARFIINDWVTKHTKGMISNLQKGAV	180

121	FVQRDLKLVQGFMPHFFRLFRSTYKQVDSEVERARFLFNDWVKTHTKSM1SNUJGKAV	180
181	DQLTRVLVNAVLFGNQWKTPFDPSITHRRLFKHSDGSTVSVPMMACTNKFKNTYTFETTPD	240

181	DQLTRLVLNVALYFGQWKTTPPSSTHRLFLFKSDGTSVSPVMMAQTMKFNYTIEFTPTD
184	GHYDIDLEPYKGDTLSMPIAAYPKVEYKPLSALTNTILSAQLISHWKGMTRLPRLVLVPK
240	300

241 GHYDILEPYYGDDLSMFIAAPYEKEVPLSALTNIILSAQLISHWKGNNTRLPRLLVLPK 300
301 FSLETEVDLARKPLNLGMWDMEROQADTSLSDQEPLHVAQALQKVKEVNESCTVASS 360

301 FSLETEVDLERKPLNLGHTDMFRQOQADFTSLSDQEPLHVAOLQKVKEVNNESSTVASS 360
361 STAVIVSARNAMAPEETIMDRPFLFVRHNPNTGTVLFGQVMEP 402
362 STAVIVSARNAMAPEETIMDRPFLFVRHNPNTGTVLFGQVMEP 402

CC or preventing arthritis caused by degenerative joint disease, preferably rheumatoid arthritis, psoriatic arthritis, infectious arthritis, juvenile rheumatoid arthritis, osteoarthritis, and spondyloarthropathies in a mammal, especially a human. It is also useful for identifying agents for treating or preventing arthritis in a mammal and it is also useful in antisense-therapy and antibody therapy. The present sequence is human PAI -1 protein

XX Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 6; Length 402;

Best Local Similarity 100.0%; Pred. No. 4.4e-190; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ 1 MQMSPALTCVLVGLALVPGEGSAVHPPSYTAHLASDFGRVFEQVAQASKDRNVTFSPY 60

Db 1 MQMSPALTCVLVGLALVPGEGSAVHPPSYVAHLASDFGRVFEQVAQASKDRNVTFSPY 60

Qy 61 GVASVIALMLQLQTGGTQQTOAAMGFKIDDKGMAPALRHLYKELMGPWNKDELTSTDAI 120

Db 61 GVASVIALMLQLQTGGTQQTOAAMGFKIDDKGMAPALRHLYKELMGPWNKDELTSTDAI 120

Qy 121 FVQRDLKLVQGFMPHPFLFRSTVKQDFSEVERARFINDWVKHTKGKMSNLIGKGA 180

Db 121 FVQRDLKLVQGFMPHPFLFRSTVKQDFSEVERARFINDWVKHTKGKMSNLIGKGA 180

Qy 181 DQLTRLVLVNLAYENGQWKTPEPDSSTTHRLFKSDGSTSVPFLKSDGSTSVPFLK 240

Db 181 DQLTRLVLVNLAYENGQWKTPEPDSSTTHRLFKSDGSTSVPFLKSDGSTSVPFLK 240

Qy 241 GHYYDILELPHGDTLSMFIAPYEKEVPLSALTNTLSAQLI SHWKGNMTLPRLLVLPK 300

Db 241 GHYYDILELPHGDTLSMFIAPYEKEVPLSALTNTLSAQLI SHWKGNMTLPRLLVLPK 300

Qy 301 FSLETEVDLRLKPLENIGMTDMFRQFQADFTSLSDQEPHYAQLQKVKIEVNESGTVA 360

Db 301 FSLETEVDLRLKPLENIGMTDMFRQFQADFTSLSDQEPHYAQLQKVKIEVNESGTVA 360

Qy 361 STAVIVSARMAPEEETIMDRPFLFVHNPPTGTVLFMGQMEP 402

Db 361 STAVIVSARMAPEEETIMDRPFLFVHNPPTGTVLFMGQMEP 402

RESULT 8 ABR82199

ID ABR82199 Standard; protein; 402 AA.

AC ABR82199;

XX DT 30-SEP-2003 (first entry)

XX DE Human plasminogen activator inhibitor 1 (PAI-1).

XX KW Human: plasminogen activator inhibitor; PAI-1; PAI; proteinase inhibitor;

XX KW mutant: proteinase inhibitor.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1 ..23

FT FT /label= signal

FT Protein 24 ..402

FT FT /label= PAI-1

/note= "plasminogen activator inhibitor 1"

XX WO2003053921-A2.

XX PD 03-JUL-2003.

XX XX 18-JUL-2002; 2002WO-US022822.

XX PR 18-JUL-2001; 2001US-0305908P.

XX XX

(AMIA-) AMERICAN NAT RED CROSS.

XX Lawrence DA, Gorlatova N, Crandall DL;

XX WPI:2003-569214/53.

DR DR-NPSDB; ACP06144.

XX Novel mutant proteinase inhibitor comprising a mutation in an epitope of a wild type proteinase inhibitor, useful for screening compounds that affect inhibitory activity of the proteinase inhibitor.

XX Claim 8; Fig 1; 46pp; English.

XX PS Sequence 402 AA;

CC The present invention describes a mutant proteinase inhibitor (I) comprising a wild-type proteinase inhibitor amino acid sequence with at least 1 mutation in at least 1 epitope of the amino acid sequence, where the mutation alters the binding of the mutant proteinase inhibitor to an anti-proteinase inhibitor antibody as compared to the binding of the wild-type proteinase inhibitor to the anti-proteinase inhibitor antibody. (I) is useful for screening at least one compound that affects the activity of a proteinase inhibitor. (I) is also useful for screening at least one compound that affects the inhibitory activity of a proteinase inhibitor. The present sequence represents human plasminogen activator inhibitor 1 (PAI-1), which is used in an example from the present invention

XX SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 6; Length 402; Best Local Similarity 100.0%; Pred. No. 4.4e-190; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Query 1 MQMSPALTCVLVGLALVPGEGSAVHPPSYVAHLASDFGRVFEQVAQASKDRNVTFSPY 60

Db 1 MQMSPALTCVLVGLALVPGEGSAVHPPSYVAHLASDFGRVFEQVAQASKDRNVTFSPY 60

Qy 61 GVASVIALMLQLQTGGTQQTOAAMGFKIDDKGMAPALRHLYKELMGPWNKDELTSTDAI 120

Db 61 GVASVIALMLQLQTGGTQQTOAAMGFKIDDKGMAPALRHLYKELMGPWNKDELTSTDAI 120

Qy 121 FVQRDLKLVQGFMPHPFLFRSTVKQDFSEVERARFINDWVKHTKGKMSNLIGKGA 180

Db 121 FVQRDLKLVQGFMPHPFLFRSTVKQDFSEVERARFINDWVKHTKGKMSNLIGKGA 180

Qy 181 DQLTRLVLVNLAYENGQWKTPEPDSSTTHRLFKSDGSTSVPFLKSDGSTSVPFLK 240

Db 181 DQLTRLVLVNLAYENGQWKTPEPDSSTTHRLFKSDGSTSVPFLKSDGSTSVPFLK 240

Qy 241 GHYYDILELPHGDTLSMFIAPYEKEVPLSALTNTLSAQLI SHWKGNMTLPRLLVLPK 300

Db 241 GHYYDILELPHGDTLSMFIAPYEKEVPLSALTNTLSAQLI SHWKGNMTLPRLLVLPK 300

Qy 301 FSLETEVDLRLKPLENIGMTDMFRQFQADFTSLSDQEPHYAQLQKVKIEVNESGTVA 360

Db 301 FSLETEVDLRLKPLENIGMTDMFRQFQADFTSLSDQEPHYAQLQKVKIEVNESGTVA 360

Qy 361 STAVIVSARMAPEEETIMDRPFLFVHNPPTGTVLFMGQMEP 402

Db 361 STAVIVSARMAPEEETIMDRPFLFVHNPPTGTVLFMGQMEP 402

RESULT 9 ABR83123

ID ABR83123 standard; protein; 402 AA.

AC ABR83123;

XX DT 18-DEC-2003 (first entry)

XX DE Human plasminogen activator inhibitor 1.

XX KW Plasminogen activator inhibitor 1; PAI-1; human; transgenic;

XX KW thrombolytic; antiasthmatic; antiinflammatory; nootropic;

KW	neuroprotective; antidepressant; nephrotropic; vulnerability; antieborheic; dermatological; antiarteriosclerotic; hepatotropic.	Qy	301 FSLPTEVDLRLKPLENLGNTDMFQEQADFTSLSLDQEPLHVAQLQKVIEVNESGGTVASS 360	XX	
KW		Db	301 FSLPTEVDLRLKPLENLGNTDMFQEQADFTSLSLDQEPLHVAQLQKVIEVNESGGTVASS 360		
Homo sapiens.		Qy	361 STAVIVSARMAPEEIMDRPFLFVRNAPTGTVLFMGQVMEP 402	XX	
OS		Db	361 STAVIVSARMAPEEIMDRPFLFVRNAPTGTVLFMGQVMEP 402		
XX	WO2003071267-A1.				
PN					
XX	PD 28-AUG-2003.				
PF	19-FBB-2003; 2003WO-US005008.				
XX	19-FBB-2002; 2002US-0358061P.				
PR					
XX	(UYVA-) UNIV VANDERBILT.				
PA	(DEC1/) DECLERCK P J.				
PA					
XX	Treating a warm-blooded vertebrate animal having a medical condition, e.g. Alzheimer's disease, atherosclerosis, myelofibrosis or glomerulosclerosis, comprises administering a plasminogen activator inhibitor-1 inhibitor.				
PT	WPI: 2003-721694/68.				
PT	DR: N-PSDB; ACF79438/ .				
XX	Disclosure: Page 62-64; 91pp; English.				
CC	The present sequence is the protein sequence of human plasminogen activator inhibitor-1 (PAI-1). The PAI-1 gene can be used to produce transgenic animals of the invention, useful for screening potential PAI-1 inhibitors. Such PAI-1 inhibitors can be used to treat a warm-blooded vertebrate animal having a medical condition, e.g. alopecia, undesired weight loss, Alzheimer's disease, systemic amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne, atherosclerosis, ageing, or a wound (claimed). A method of testing a candidate composition for PAI-1 inhibition activity comprises administering the composition to a transgenic animal having a PAI-1 gene incorporated into its genome, and observing an ameliorating change in the animal indicative of inhibition of PAI-1 activity, the change being an improvement of a vascular thrombotic disorder, asthma, chronic obstructive pulmonary disease, alopecia, undesired weight loss such as anorexia, Alzheimer's disease, systemic amyloid deposition, systemic amyloidosis, myelofibrosis, glomerulosclerosis, male pattern baldness, keloids, apocrine cysts, acne, atherosclerosis, ageing, or a wound (claimed) hepatosplenomegaly, extramedullary haematopoiesis, or a wound (claimed).				
CC	Sequence 402 AA;				
CC	Score 2071; DB 7; Length 402;				
CC	Best Local Similarity 100.0%; Pred. No. 4-4e-190; Indels 0; Gaps 0;				
CC	Matches 402; Conservative 0; Mismatches 0; Insertions 0; Gaps 0;				
Qy	1 MQMSPALTCLVLGLALVPGEGSAVHHPSYYVAHLASDFGVRYFQQVQAASKDRNVYFSPY 60				
Db	1 MQMSPALTCLVLGLALVPGEGSAVHHPSYYVAHLASDFGVRYFQQVQAASKDRNVYFSPY 60				
Qy	61 GVASVLAMQLQTGGTQQIQAMGFKIDDGKMAPARLHYKELMGPNKDEBISITDAI 120				
Db	61 GVASVLAMQLQTGGTQQIQAMGFKIDDGKMAPARLHYKELMGPNKDEBISITDAI 120				
Qy	121 FVORDLKLVQGEMPHFFPLFRSTYKQDFSEYERARFLINDWVKTHTKGMIISNLLGKAV 180				
Db	121 FVORDLKLVQGEMPHFFPLFRSTYKQDFSEYERARFLINDWVKTHTKGMIISNLLGKAV 180				
Qy	181 DQLTRIVLNALYNGQKTPPEFDSSTHRLFKHSQDGSSTVSYMMAQTKENYTFETTPD 240				
Db	181 DQLTRIVLNALYNGQKTPPEFDSSTHRLFKHSQDGSSTVSYMMAQTKENYTFETTPD 240				
Qy	Query Match 100.0%; Score 2071; DB 7; Length 402;				
Qy	Best Local Similarity 100.0%; Pred. No. 4-4e-190; Indels 0; Gaps 0;				
Db	Matches 402; Conservative 0; Mismatches 0; Insertions 0; Gaps 0;				
Qy	1 MQMSPALTCLVLGLALVPGEGSAVHHPSYYVAHLASDFGVRYFQQVQAASKDRNVYFSPY 60				
Qy	241 GHYDILELPYHGDTLSMIAAPKEVPLPSALTNIISQLSHWKGMTRPLRLLVLPK 300				
Db	241 GHYDILELPYHGDTLSMIAAPKEVPLPSALTNIISQLSHWKGMTRPLRLLVLPK 300				

Page 8

PD 23-OCT-2003.
 XX 23-APR-2002; 2002US-00128706.
 PP 23-APR-2002; 2002US-00128706.
 XX (ITES/) ITESCU S.
 PA (ITES/) ITESCU S.
 XX
 PI Itescu S;
 XX WPI: 2003-852809/79.
 DR N-PSDB; AAD64654, AAD64654.
 XX New catalytic nucleic acid that hybridizes to and specifically cleaves an mRNA encoding a Plasminogen Activator Inhibitor-1, useful in preparing a composition for treating e.g., cardiovascular or fibrotic disease.
 XX Disclosure; SEQ ID NO 6; opp; English.
 XX The present invention relates to a new catalytic nucleic acid that hybridizes to and specifically cleaves a plasminogen activator inhibitor-1 (PAI-1). The invention is useful in preparing a composition for treating cardiovascular or fibrotic disease. The invention is also used in gene therapy. The present sequence is human plasminogen activator inhibitor-1 (PAI-1) protein
 CC Sequence 402 AA;
 SQ Query Match 100.0%; Score 2071; DB 7; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 402;
 Db 1 MQMSPALTCLVGLALVFGESAVHPPSTYAHLASDFGRVFOQVAQASKDKNVFSPY 60
 Qy 1 MQMSPALTCLVGLALVFGESAVHPPSTYAHLASDFGRVFOQVAQASKDKNVFSPY 60
 Db 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Qy 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Db 61 GVASHVLLMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Qy 121 FVQRDLKLVQGMMPHFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMTISNLJLGKAV 180
 Db 121 FVQRDLKLVQGMMPHFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMTISNLJLGKAV 180
 Qy 181 DQLTRLVNLYENGKWTPEPDSSTTHRLFKSDGSTVSVPVMAQTKENYNTETFTPD 240
 Db 181 DQLTRLVNLYENGKWTPEPDSSTTHRLFKSDGSTVSVPVMAQTKENYNTETFTPD 240
 Db 121 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Qy 241 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Db 241 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Qy 301 FSLETEVDLRKELENLGMTDMFQOFDFTSLSDQEPHYAQALQKVIEVNESGTVASS 360
 Db 301 FSLETEVDLRKELENLGMTDMFQOFDFTSLSDQEPHYAQALQKVIEVNESGTVASS 360
 RESULT 13
 ADN95544 ID ADN95544 standard; protein; 402 AA.
 XX AC ADN95544;
 XX DT 01-JUL-2004 (First entry)
 DE Human BEC/LEC-related protein sequence SeqID467.
 XX growth, differentiation; blood endothelial cell; BBC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema;
 VEGFR-3;

KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
 KW vasoconstrictive; antiinflammatory; gene therapy; endothelial cell disorder;
 KW inflammatory disease; cancer metastasis; lymphatic system; human.
 XX Homo sapiens.
 OS XX
 PN WO2003080640-A1.
 XX PD 02-OCT-2003.
 XX PR 07-MAR-2003; 2003WO-US06900.
 PF 07-MAR-2003; 2003WO-US06900.
 XX PR 07-MAR-2002; 2002US-0363019P.
 XX PA (LUDWIG) LUDWIG INST CANCER RES.
 PA (LICENTIA) LICENTIA LTD.
 PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
 XX WPI: 2003-876699/81.
 DR N-PSDB; ADN95545.
 XX Example 1; SEQ ID NO 467; 176pp; English.
 PS XX
 CC This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprising contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasoconstrictive or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for compounds with an antiangiogenic, cytostatic, vasoconstrictive or antiinflammatory activity or for gene therapy. The method is useful in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed protein which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.

SQ Sequence 402 AA;
 Query Match 100.0%; Score 2071; DB 7; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 402;
 Db 1 MQMSPALTCLVGLALVFGESAVHPPSTYAHLASDFGRVFOQVAQASKDKNVFSPY 60
 Qy 1 MQMSPALTCLVGLALVFGESAVHPPSTYAHLASDFGRVFOQVAQASKDKNVFSPY 60
 Db 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Qy 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Db 61 GVASHVLLMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Qy 121 FVQRDLKLVQGMMPHFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMTISNLJLGKAV 180
 Db 121 FVQRDLKLVQGMMPHFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMTISNLJLGKAV 180
 Db 121 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Qy 241 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Db 241 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Qy 301 FSLETEVDLRKELENLGMTDMFQOFDFTSLSDQEPHYAQALQKVIEVNESGTVASS 360
 Db 301 FSLETEVDLRKELENLGMTDMFQOFDFTSLSDQEPHYAQALQKVIEVNESGTVASS 360
 SQ Sequence 402 AA;
 Query Match 100.0%; Score 2071; DB 7; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MQMSPALTCLVGLALVFGESAVHPPSTYAHLASDFGRVFOQVAQASKDKNVFSPY 60
 Qy 1 MQMSPALTCLVGLALVFGESAVHPPSTYAHLASDFGRVFOQVAQASKDKNVFSPY 60
 Db 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Qy 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Db 61 GVASVIALMLQLTTGGTQQIQAANGFKIDDKGMAPALRLYKELMGPWNKDEISTDAI 120
 Qy 121 FVQRDLKLVQGMMPHFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMTISNLJLGKAV 180
 Db 121 FVQRDLKLVQGMMPHFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMTISNLJLGKAV 180
 Qy 181 DQLTRLVNLYENGKWTPEPDSSTTHRLFKSDGSTVSVPVMAQTKENYNTETFTPD 240
 Db 181 DQLTRLVNLYENGKWTPEPDSSTTHRLFKSDGSTVSVPVMAQTKENYNTETFTPD 240
 Db 121 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Qy 241 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Db 241 GHYYDILPLPHGTDSLMSMFIAYPEKEPVISALTNLISAQLISSHWKGNMTPLPRLVLPK 300
 Qy 301 FSLETEVDLRKELENLGMTDMFQOFDFTSLSDQEPHYAQALQKVIEVNESGTVASS 360
 Db 301 FSLETEVDLRKELENLGMTDMFQOFDFTSLSDQEPHYAQALQKVIEVNESGTVASS 360
 RESULT 13
 ADN95544 ID ADN95544 standard; protein; 402 AA.
 XX AC ADN95544;
 XX DT 01-JUL-2004 (First entry)
 DE Human BEC/LEC-related protein sequence SeqID467.
 XX growth, differentiation; blood endothelial cell; BBC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema;
 VEGFR-3;

DR N-PSDB; ADL35811.
 XX 16-AUG-1996; 96US-0024056P.
 PT 15-AUG-1997; 97US-00314011.
 PT 19-FEB-1998; 98US-00026408.
 PT 12-JUL-2001; 2001US-00902684.
 XX
 PA (NIJUS/); NI J.
 PA (GENTZ/); GENTZ R L.
 PA (RUBEN/); RUBEN S M.
 PA (SHRY/); SHI Y E.
 XX
 PI Ni J, Gentz RL, Ruben SM, Shi YE;
 XX
 DR WPI; 2004-356204/33.
 XX Producing an antibody that specifically binds to pancreas-derived
 PT plasminogen activator inhibitor (PAI) polypeptide comprises introducing
 PT the polypeptide to the animal, and recovering the antibody.
 XX Disclosure; SEQ ID NO 3; 51pp; English.
 XX
 CC The present invention provides pancreas-derived plasminogen activator
 CC inhibitor (PAI) polypeptides and their encoding polynucleotides. The
 CC invention is useful for producing an antibody that specifically binds to
 CC pancreas-derived plasminogen activator inhibitor (PAI) polypeptide. The
 CC present sequence is human plasminogen activator inhibitor (PAI) protein.
 XX Sequence 402 AA:
 XX
 Query Match 100.0%; Score 2071; DB 8; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4-4e-190;
 Matches 402; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;
 SQ 1 M Q M P A I T C L V G L A L V F G E G S A V H R H P P S Y A H L A S D F G V R V F Q Q V A Q A S K D R N V F S P Y 60
 Db 1 M Q M P A I T C L V G L A L V F G E G S A V H R H P P S Y A H L A S D F G V R V F Q Q V A Q A S K D R N V F S P Y 60
 Db 61 G V A S V L A M I Q L T T G E T Q Q I Q A M G F K I D D K G M A P A L R H Y K E L M G P W N K D E I S T T D A I 120
 Db 61 G V A S V L A M I Q L T T G E T Q Q I Q A M G F K I D D K G M A P A L R H Y K E L M G P W N K D E I S T T D A I 120
 Db 121 F V Q R D L K V Q G F M P H F P L F R S T V K Q D F S E V E R A R P I I N D W K T H T K G M I S N L L G K A V 180
 Db 121 F V Q R D L K V Q G F M P H F P L F R S T V K Q D F S E V E R A R P I I N D W K T H T K G M I S N L L G K A V 180
 Qy 181 D O L T R L V I N A L X F G N Q M K T P P D S S T R R L F H K D G S T V S P M M A Q T N K E N Y T E F T P D 240
 Db 181 D Q T R L V I N A L X F G N Q M K T P P D S S T R R L F H K D G S T V S P M M A Q T N K E N Y T E F T P D 240
 Qy 241 G H Y D I L L P V H G D T L S M F I A A P Y E K V P L S A L T N I L S A Q L I S H W K G M N T R L P R I L V L P K 300
 Db 241 G H Y D I L L P V H G D T L S M F I A A P Y E K V P L S A L T N I L S A Q L I S H W K G M N T R L P R I L V L P K 300
 Qy 301 F S L E T E V D L R K P L E N I G D M F R Q O A D F T S I S D Q E P H V A L Q O L R K V I E V N E S G T V A S S 360
 Db 301 F S L E T E V D L R K P L E N I G D M F R Q O A D F T S I S D Q E P H V A L Q O L R K V I E V N E S G T V A S S 360
 Qy 361 S T A V I S S A R M A P E E I T M D R P L F V R H R N P T G T V L F M G Q V M E P 402
 Db 361 S T A V I S S A R M A P E E I T M D R P L F V R H R N P T G T V L F M G Q V M E P 402
 RESLT 16
 ID ADO05046 standard; protein; 402 AA.
 XX Plasminogen activator inhibitor; PAI; human.
 AC ADO05046;
 DT 29-JUL-2004 (first entry)
 XX Human plasminogen activator inhibitor (PAI)-1 protein.
 XX Plasminogen activator inhibitor; PAI; human.
 OS Homo sapiens.
 PN US2004066978-A1.
 XX 06-MAY-2004.
 XX 29-JUL-2003; 2003US-00628395.
 PF RESULT 17
 ABM80915
 ID ABM80915 Standard; protein; 402 AA.
 XX AC ABM80915;
 XX DT 18-NOV-2004 (first entry)
 XX Tumour-associated antigenic target (TAT) polypeptide PRO2604, SEQ:2362.
 DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;

KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW chromosome identification; melanoma; leukaemia; hybridisation probe;
 KW gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2004030615-A2.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR WPI; 2004-347951/32.
 XX
 N-PSDB; ACN38630.
 XX
 New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS SEQ ID NO 2362; 7273pp; English.
 XX
 The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid, an antibody specific for a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention.
 XX
 Sequence 402 AA:
 XX
 Query Match 100.0%; Score 2071; DB 8; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4..4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQMSPALTCVGLAVGEGSAVHPYPSVYAHLSDFGRVFOQVAQASKDRNVFSPPY 60
 Db 1 MQMSPALTCVGLAVGEGSAVHPYPSVYAHLSDFGRVFOQVAQASKDRNVFSPPY 60
 Qy 61 GVASYLAMLOLTGGGBTQQOQAAMGFKDDKGKMAPALRHLYKELMGPWNKDEISSLTDAI 120
 Db 61 GVASYLAMLOLTGGGBTQQOQAAMGFKDDKGKMAPALRHLYKELMGPWNKDEISSLTDAI 120
 Qy 121 FVQRDLKLYQGMPMPFFRFLRSTVQDSEVERARFLINDWIKTHTKGMISNLGKGAV 180
 Db 121 FVQRDLKLYQGMPMPFFRFLRSTVQDSEVERARFLINDWIKTHTKGMISNLGKGAV 180
 Qy 181 DQLTRLVLVNLALYFNGWIKTPPDSSTHRLFKSDGTSVPMNAQTNKFNTEFTTD 240
 Db 181 DQLTRLVLVNLALYFNGWIKTPPDSSTHRLFKSDGTSVPMNAQTNKFNTEFTTD 240

241 GHYYDILELPYHGDTLSMPTIAAPYKEYVPLSALTNTILSQAQLISHWKGNMTRLPPLVLPK 300
 241 GHYYDILELPYHGDTLSMPTIAAPYKEYVPLSALTNTILSQAQLISHWKGNMTRLPPLVLPK 300
 301 FSLETEVDLRKPLENLGMDMFRQFQADTSLSQOPLHVAQLOKVKEVNESGTVAASS 360
 301 FSLETEVDLRKPLENLGMDMFRQFQADTSLSQOPLHVAQLOKVKEVNESGTVAASS 360
 Qy 361 STAVIVSARMAPPEEIMDRPFLFVTRHNPTGTVLFMGQYMEP 402
 Db 361 STAVIVSARMAPPEEIMDRPFLFVTRHNPTGTVLFMGQYMEP 402
 RESULT 18
 ADP23374
 ID ADP23374 standard; protein; 402 AA.
 XX
 AC ADP23374;
 XX
 DT 18-NOV-2004 (first entry)
 DE PRO polypeptide SEQ ID NO:552.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 OS Unidentified.
 XX
 PN WO2004041170-A2.
 XX
 PD 21-MAY-2004.
 XX
 PR 30-OCT-2003; 2003WO-US034312.
 XX
 PR 01-NOV-2002; 2002US-0423394P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 PI PI
 Wu TD;
 XX
 DR WPI; 2004-419628/39.
 XX
 New polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoïd arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 XX
 PS SEQ ID NO 552; 294pp; English.
 XX
 The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC anti-inflammatory, antiarthritic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, anti-allergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immunological disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis,
 CC idiopathic inflammatory myopathy, Sjögren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin

CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic CC disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity CC pneumonitis, a transplant-associated disease, graft rejection or CC graft-versus-host disease. The present sequence represents a PRO protein CC of the invention.

XX Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 8; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 1 NQMSPA[L]C[V]GLA[V]FGE[S]AVH[H]P[S]TVAHLASDFGRV[F]RQQAQS[K]D[R]N[V]FSSY 60
 Db 1 NQMSPA[L]C[V]GLA[V]FGE[S]AVH[H]P[S]TVAHLASDFGRV[F]RQQAQS[K]D[R]N[V]FSPY 60
 Qy 61 GVASV[AL]MQLQTGGETQQIQAANGFKIDDGKMAPALRLYKELMGPKNKE[ST]DAI 120
 Db 61 GVASV[AL]MQLQTGGETQQIQAANGFKIDDGKMAPALRLYKELMGPKNKE[ST]DAI 120
 Qy 121 FVQRDLKLVQGFM[P]HFRFLFSTVKQDFSEVERAFIN[D]WVKT[K]GMINL[G]KAV 180
 Db 121 FVQRDLKLVQGFM[P]HFRFLFSTVKQDFSEVERAFIN[D]WVKT[K]GMINL[G]KAV 180
 Qy 181 DQLTRLV[V]NALLYFNGQWKT[P]RDSSTTHRLFKSDGSTSV[P]VMAQTKNFNT[E]FTTPD 240
 Db 181 DQLTRLV[V]NALLYFNGQWKT[P]RDSSTTHRLFKSDGSTSV[P]VMAQTKNFNT[E]FTTPD 240
 Qy 241 GHYYDILELPYHGDTLSMFIAYPEKEVPLSALTNLISQ[LI]SHKG[GN]TRLPRLLVLPK 300
 Db 241 GHYYDILELPYHGDTLSMFIAYPEKEVPLSALTNLISQ[LI]SHKG[GN]TRLPRLLVLPK 300
 Qy 301 FSLETEVDLRKPLENIGMTDMFQADFITSLSDQEPLHYAQALQKVIEVNE[SG]TVASS 360
 Db 301 FSLETEVDLRKPLENIGMTDMFQADFITSLSDQEPLHYAQALQKVIEVNE[SG]TVASS 360
 Qy 361 STAVIVSARMAPBEITIMDRPFLFVWHPNPTCVYLENGQMEP 402
 Db 361 STAVIVSARMAPBEITIMDRPFLFVWHPNPTCVYLENGQMEP 402
 XX

RESULT 19
 ADQ39257 standard; protein; 402 AA.
 XX
 AC ADQ39257;
 DT 18-NOV-2004 (First entry)
 DB Human myocardial infarction-associated gene derived protein, SEQ ID 920.
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiact; gene therapy; human.
 XX
 OS Homo sapiens.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PR 22-DEC-2003; 2003WO-US040978.
 XX
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453138P.
 PR 30-APR-2003; 2003US-0466412P.
 PR 23-SEP-2003; 2003US-0504955P.
 PA (APPL-) APPLERA CORP.
 PI Cargill, M., Devin, J.J., Iakoubova, O.;
 XX
 PS ID NO 920; 145PP; English.
 XX
 The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiotropic activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 402 AA;

Query Match 100.0%; Score 2071; DB 8; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.4e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPA[L]C[V]GLA[V]FGE[S]AVH[H]P[S]TVAHLASDFGRV[F]RQQAQS[K]D[R]N[V]FSPY 60
 Db 1 MQMSPA[L]C[V]GLA[V]FGE[S]AVH[H]P[S]TVAHLASDFGRV[F]RQQAQS[K]D[R]N[V]FSPY 60
 Qy 61 GVASV[AL]MQLQTGGETQQIQAANGFKIDDGKMAPALRLYKELMGPKNKE[ST]DAI 120
 Db 61 GVASV[AL]MQLQTGGETQQIQAANGFKIDDGKMAPALRLYKELMGPKNKE[ST]DAI 120
 Qy 121 FVQRDLKLVQGFM[P]HFRFLFSTVKQDFSEVERAFIN[D]WVKT[K]GMINL[G]KAV 180
 Db 121 FVQRDLKLVQGFM[P]HFRFLFSTVKQDFSEVERAFIN[D]WVKT[K]GMINL[G]KAV 180
 Qy 181 DQLTRLV[V]NALLYFNGQWKT[P]RDSSTTHRLFKSDGSTSV[P]VMAQTKNFNT[E]FTTPD 240
 Db 181 DQLTRLV[V]NALLYFNGQWKT[P]RDSSTTHRLFKSDGSTSV[P]VMAQTKNFNT[E]FTTPD 240
 Qy 241 GHYYDILELPYHGDTLSMFIAYPEKEVPLSALTNLISQ[LI]SHKG[GN]TRLPRLLVLPK 300
 Db 241 GHYYDILELPYHGDTLSMFIAYPEKEVPLSALTNLISQ[LI]SHKG[GN]TRLPRLLVLPK 300
 Qy 301 FSLETEVDLRKPLENIGMTDMFQADFITSLSDQEPLHYAQALQKVIEVNE[SG]TVASS 360
 Db 301 FSLETEVDLRKPLENIGMTDMFQADFITSLSDQEPLHYAQALQKVIEVNE[SG]TVASS 360
 Qy 361 STAVIVSARMAPBEITIMDRPFLFVWHPNPTCVYLENGQMEP 402
 Db 361 STAVIVSARMAPBEITIMDRPFLFVWHPNPTCVYLENGQMEP 402
 XX
 RESULT 20

ADDQ39256	standard; protein; 402 AA.	Db	1 MQMSPALTCVLGLALVFCBGSAYHPPSYVAHLASDFGVRFQQVAQASKDRNVFSPY 60
ID		Qy	61 GVASVTLAMQLQTTGEGTQQQIAQAMGFKIDDKGMAPALRHLYKELMGPMNKDEISTTDAL 120
AC	ADQ39256;	Db	61 GVASVTLAMQLQTTGEGTQQQIAQAMGFKIDDKGMAPALRHLYKELMGPMNKDEISTTDAL 120
XX		Qy	
DT	18-NOV-2004 (First entry)	Db	121 FVQRDLKLIVQGFMMPFFRLFRSTYKVQDFSEVERARFLINDWYKTHKGMISNLGKGAV 180
XX		Qy	
DE	Human myocardial infarction-associated gene derived protein, SEQ ID 919.	Db	121 FVQRDLKLIVQGFMMPFFRLFRSTYKVQDFSEVERARFLINDWYKTHKGMISNLGKGAV 180
XX		Qy	
KW	Myocardial infarction; detection; single nucleotide polymorphism; SNP;	Db	121 FVQRDLKLIVQGFMMPFFRLFRSTYKVQDFSEVERARFLINDWYKTHKGMISNLGKGAV 180
XX		Qy	
XX	cardiant; gene therapy; human.	Db	181 DQLTRLVNLVNLFGNGKTPFPDSSTARLFLFKSDGSTSVPMMAQTNKFNTEFTPD 240
OS	Homo sapiens.	Db	181 DQLTRLVNLVNLFGNGKTPFPDSSTARLFLFKSDGSTSVPMMAQTNKFNTEFTPD 240
XX		Qy	
PN	WO2004055052-A2.	Db	241 GHYYDILELPYHGDTLSMFIAPPKEYPLSALTNILSAQIHLNTRPLRLLVLPK 300
XX		Qy	
PD	15-JUL-2004.	Db	241 GHYYDILELPYHGDTLSMFIAPPKEYPLSALTNILSAQIHLNTRPLRLLVLPK 300
XX		Qy	
PF	22-DBC-2003; 2003W0-US040978.	Db	301 FSLETEVDLRKPLLENGLMTDMFQFQADFTSLSDQEPLHVAQQLQKVKEVNESGTVA 360
XX		Qy	
PR	20-DEC-2002; 2002US-0434778P.	Db	301 FSLETEVDLRKPLLENGLMTDMFQFQADFTSLSDQEPLHVAQQLQKVKEVNESGTVA 360
PR	10-MAR-2003; 2003US-0453135P.	Qy	361 STAVIVSARMAPERIMDRPFLTVRNPTGTVLFMGQYMEP 402
PR	30-APR-2003; 2003US-0465412P.	Db	361 STAVIVSARMAPERIMDRPFLTVRNPTGTVLFMGQYMEP 402
PR	23-SEP-2003; 2003US-0504955P.	Qy	
XX		Db	
(APPL-)	APPLERA CORP.	XX	
XX		RESULT 21.	
PI	Cargill M, Devlin JJ, Takoobova O;	XX	ADV70216 standard; protein; 402 AA.
XX		XX	ADV70216;
DR	WPI; 2004-533949/51.	XX	AC ADV70216;
DR	N-PDBB; ADQ3B428.	XX	10-MAR-2005 (first entry)
XX		XX	Tumor-associated antigenic target polypeptide TAT458.
PT	Identifying an individual who has an altered risk for developing a single nucleotide polymorphism in	XX	
PT	myocardial infarction by detecting a single nucleotide polymorphism in	XX	
PT	the individual's nucleic acids.	XX	
XX		XX	Cytostatic; diagnosis; therapy; tumor;
XX		XX	tumor-associated antigenic target polypeptide; TAT.
XX		XX	Homo sapiens.
XX		XX	WO2004112829-A2.
XX		XX	29-DEC-2004.
XX		XX	21-MAY-2004; 2004WO-US016121.
XX		XX	23-MAY-2003; 2003US-0473238P.
XX		XX	27-FEB-2004; 2004US-0548299P.
XX		XX	(GETH) GENENTECH INC.
XX		XX	Phillips H;
XX		XX	WPI; 2005-048766/05.
CC	The invention relates to a novel method for identifying an individual who	XX	DR N-PDBB; ADV70121.
CC	has an altered risk for developing myocardial infarction. The method	XX	
CC	comprises detecting a single nucleotide polymorphism (SNP) in any one of	XX	
CC	the nucleotide sequences given in the specification in the individual's	XX	
CC	nucleic acids, where the presence of the SNP is correlated with an	XX	
CC	altered risk for myocardial infarction in the individual. The invention	XX	
CC	further comprises an isolated nucleic acid molecule comprising at least	XX	
CC	8 contiguous nucleotides where one of the nucleotides is an SNP given in	XX	
CC	the specification or its complement and encoding any one of the amino	XX	
CC	acid sequences given in the specification; an isolated polypeptide	XX	
CC	comprising an amino acid sequence given in the specification; an antibody	XX	
CC	that specifically binds to the polypeptide or its antigen-binding	XX	
CC	fragment; an amplified polynucleotide containing an SNP given in the	XX	
CC	specification and which is between about 16 and 100 nucleotides in	XX	
CC	length; a kit for detecting an SNP in a nucleic acid, comprising the	XX	
CC	polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a	XX	
CC	nucleic acid molecule; a method of detecting a variant polypeptide;	XX	
CC	a method for identifying an agent useful in treating or preventing	XX	
CC	myocardial infarction. The novel detection method has cardiac activity.	XX	
CC	The nucleic acids of the invention may be used in gene therapy. The	XX	
CC	method is useful in identifying an individual who has an increased or	XX	
CC	decreased risk for developing myocardial infarction and for preparing a	XX	
CC	composition for treating or preventing myocardial infarction. This	XX	
CC	sequence represents the protein of a human myocardial infarction-	XX	
CC	associated gene containing one or more SNP's of the invention. Note: This	XX	
CC	sequence was not shown in the specification. The sequence has come from	XX	
CC	an electronic sequence listing downloaded from the WIPO website.	XX	
CC	Sequence 402 AA;	XX	
SQ	Query Match 100.0%; Score 2071; DB 8; Length 402;		
	Best Local Similarity 100.0%; Pred. No. 4.4e-190;		
	Mismatches 0; Indels 0; Gaps 0;		
	Matches 402; Conservative 0;		
	1 MQMSPALTCVLGLALVFCBGSAYHPPSYVAHLASDFGVRFQQVAQASKDRNVFSPY 60		

mammal. The method is useful in creating a mammal having a tumor of glial origin comprising cells that express a type A or B glial tumor antigen. This sequence represents a human tumor-associated antigenic target polypeptide.

Plasminogen activator inhibitor-1 (PAI-1), useful for treating vascular, thrombotic or hemostatic disorders.

Sequence 402 AA:						
	Query	Match	Score	DB 9;	Length	402;
SG		Best Local Similarity	100.0%;	Pred. No. 4.4e-190;		
Qy		Matches 402; Conservative	100.0%;	Mismatches 0;	Indels 0;	Gaps 0;
Ddb						
Qy	1	MQMSPALTCVGLALVFGEGSAVHPPSYAHLADFGYRVPQOQAQSKDRNVSFPY	60			
Ddb	1	MQMSPALTCVGLALVFGEGSAVHPPSYAHLADFGYRVPQOQAQSKDRNVSFPY	60			
Qy	61	GVASVLAMILQLITGGTGTGQQIQAAMGFKIDDKGMADPLRHLYKELMGPMWKKDEI	120	STTD	DAI	
Ddb	61	GVASVLAMILQLITGGTGTGQQIQAAMGFKIDDKGMADPLRHLYKELMGPMWKKDEI	120	STTD	DAI	
Qy	121	FVQRDLKLVQGFMHPFFPLFRSTVKQDFSEVERAFIINDWVKHTKGMSNLIGKGAV	180			
Ddb	121	FVQRDLKLVQGFMHPFFPLFRSTVKQDFSEVERAFIINDWVKHTKGMSNLIGKGAV	180			
Qy	181	DQLTRLVLYNALYFNGQWKTTPDDSSTHRRLPHKSDGSTSVPMMAQTNKENYTT	240	ETTPD		
Ddb	181	DQLTRLVLYNALYFNGQWKTTPDDSSTHRRLPHKSDGSTSVPMMAQTNKENYTT	240	ETTPD		

Qy	241	GHYDILELPYHDGDTLSMFIAAAPYEKEVPLSALTNTILSAQJSHKGNGNMTRLPRVLVPK	300
Ddb	241	GHYDILELPYHDGDTLSMFIAAAPYEKEVPLSALTNTILSAQJSHKGNGNMTRLPRVLVPK	300
Qy	301	FSLTEVDLRLKPYLENLGMTDMFQRQADFTSLSQDEBLHLVAQALQKVIEVNESTGVASS	360
Ddb	301	FSLTEVDLRLKPYLENLGMTDMFQRQADFTSLSQDEBLHLVAQALQKVIEVNESTGVASS	360
Qy	361	STATIVSARMAPEEITIMDRPFLFVRNINTPTGTIVLFMGQVMEP	402
Ddb	361	STATIVSARMAPEEITIMDRPFLFVRNINTPTGTIVLFMGQVMEP	402

RESULT 22
 AEA81039 standard; protein; 402 AA.
 ID AEA81039
 XX
 XX
 AC AEA81039;
 DT 08-SEP-2005 (first entry)
 DE Human plasminogen activator inhibitor-1 protein SEQ ID NO:6.
 XX
 XX
 XX
 KW antisense therapy; RNA interference; plasminogen activator inhibitor-1;
 KW vasoconstrictor; thrombolytic; hemostatic; vascular disease;
 KW thrombocyte disorder.
 KW

XX
 Homo sapiens.
 OS
 XX
 US2005148527-A1.
 PN
 XX
 PD
 07-FUL-2005.
 XX
 PF
 24-FEB-2005; 2005US-00512496.
 XX
 PR
 23-APR-2002; 2002US-00128706.
 PR
 23-APR-2003; 2003WO-US012767.

XX (ITES/) ITESCU S.
 XX PA
 XX PI Itescu S;
 XX WPI; 2005-478099/48.
 XX DR N-PSDB; AEA81038, AEA81050.
 XX PT New catalytic nucleic acid that specifically cleaves an mRNA encoding a

Plasminogen activator inhibitor-1 (PAI-1), useful for treating vascular, thrombotic or hemostatic disorders.

The invention relates to a catalytic nucleic acid that specifically cleaves an mRNA encoding a plasminogen activator inhibitor-1 (PAI-1). Also described: (1) a pharmaceutical composition comprising the catalytic nucleic acid, oligonucleotide, or inhibitor of PAI-1 expression, and a carrier; (2) a method of treating a cardiovascular disease in a subject; (3) a method of treating a vascular disease in a subject where the disease is treated by reducing thrombin or fibrin production; (4) a method of treating a vascular disease in a subject where the vascular disease is treated by inhibition of PAI-1 expression; (5) a method of inducing neovascularization in a heart tissue of a subject; (6) a method of inhibiting smooth muscle cell proliferation in a tissue of a subject; (7) a method of inhibiting thrombin and fibrin deposition in a heart or tissue of a subject; (8) a method of treating a subject suffering from a thrombotic disease or disorder, or hemostatic disorder where the disease or disorder is associated with elevated expression of PAI-1; and (9) a method of treating a disorder of a subject's heart involving loss of cardiomyocytes. The nucleic acid, compositions and methods are useful for treating vascular, thrombotic or hemostatic disorders. The present sequence represents human PAI-1, which is used in the exemplification of the present invention.

GenCore version 5.1.6
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OM protein - protein search, using sw model
 Run on: December 13, 2005, 09:01:15 ; Search time 47 Seconds
 (without alignments)
 707.141 Million cell updates/sec

Title: US-10-506-406-2

Perfect score: 2071

Sequence: 1 MQMSPALTCLVGLALVFGEE.....FVVRNPTGTVLFMGQYMEP 402

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Listing First 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:
 3: /cgn2_6/ptodata/1/iaa/8_COMB.pep:
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:
 6: /cgn2_6/ptodata/1/iaa/batchfile1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2071	100.0	402	1 US-08-315-461-7
2	2071	100.0	402	2 US-08-840-204-2
3	2071	100.0	402	2 US-09-056-408-3
4	2071	100.0	402	2 US-09-324-490A-2
5	2071	100.0	402	2 US-09-902-694-3
6	2071	100.0	402	2 US-10-628-395-3
7	2007	96.9	390	1 US-08-121-714-6
8	2007	96.9	390	1 US-08-417-108A-6
9	2007	96.9	390	1 US-08-477-112-6
10	2007	96.9	390	4 PCT-US93-08322-6
11	1958	94.5	379	2 US-08-840-204-3
12	1958	94.5	379	2 US-09-324-494A-3
13	1784	86.1	402	2 US-08-940-997-4
14	1784	86.1	402	2 US-09-345-817A-4
15	1794	86.1	402	2 US-09-728-292-4
16	791.5	38.2	397	2 US-08-948-997-5
17	791.5	38.2	397	2 US-09-345-817A-5
18	791.5	38.2	397	2 US-09-728-292-5
19	771.5	37.3	397	6 5187089-9
20	770.5	37.2	397	6 5457090-2
21	770.5	37.2	397	6 5495001-7
22	768.5	37.1	397	6 US-09-660-107-1
23	765.5	37.0	397	6 5187089-10
24	762.5	36.8	397	6 5457090-4
25	762	36.8	398	6 5187089-6
26	760	36.7	398	6 5495001-9
27	759.5	36.7	397	6 5187089-2

ALIGNMENTS

RESULT 1
 US-08-315-461-7
 ; Sequence 7, Application US/08315461
 ; Patient No. 5639726
 ; GENERAL INFORMATION:
 / APPLICANT: Lawrence, Daniel A.
 / APPLICANT: Ginsburg, David
 / APPLICANT: Shore, Joseph D.
 / APPLICANT: Fay, William P.
 / APPLICANT: Olson, Steven T.
 / APPLICANT: Francis-Chmura, Anne-Marie
 / APPLICANT: Dell'Elitzman
 / APPLICANT: Dell Patelii
 / TITLE OF INVENTION: Peptide Mediated Enhancement Of
 / TITLE OF INVENTION: Thrombolysis: Methods and Compositions
 / NUMBER OF SEQUENCES: 7
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Arnold, White & Durkee
 / STREET: P.O. Box 4433
 / CITY: Houston
 / STATE: TX
 / COUNTRY: USA
 / ZIP: 77210
 / COMPUTER READABLE FORM:
 / COMPUTER TYPE: Floppy disk
 / COMPUTER: IBM PC Compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/315,461
 / FILING DATE: Concurrently Herewith
 / CLASSIFICATION: 530
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Parker, David L.
 / REGISTRATION NUMBER: 32,165
 / REFERENCE/DOCKET NUMBER: UMIC:006
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (512) 418-3000
 / TELEFAX: (512) 474-5777
 / INFORMATION FOR SEQ ID NO: 7:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 402 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: Single
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-315-461-7

Query Match Similarity 100.0% ; Score 2071; DB 1; Length 402;
 Best Local Similarity 100.0% ; Pred. No. 4.6e-204;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 2071; DB 202; Length 402;
Best Local Similarity 100.0%; Pred. No. 4.6e-204;
Matches 400; MisMatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVGLALVPGESSAVHPPSYVAHLASDFGTRVFOQAQSKDRNVFSPY 60
Db 1 MQMSPALTCLVGLALVPGESSAVHPPSYVAHLASDFGTRVFOQAQSKDRNVFSPY 60
Qy 61 GVASYLAMQLQTGGTQQIQAANGFKIDDKGMAPALRHYKELMGPNKDEISTTDI 120
Db 61 GVASYLAMQLQTGGTQQIQAANGFKIDDKGMAPALRHYKELMGPNKDEISTTDI 120
Qy 121 FVQRDLKLVQGFMPIFFRLPRSTVKQDFSEVERARFLINDWVKTHTKGMIISNLJGKAV 180
Db 121 FVQRDLKLVQGFMPIFFRLPRSTVKQDFSEVERARFLINDWVKTHTKGMIISNLJGKAV 180
Qy 181 DQLTRLVNLYNALYNGQKNTPEPPIPOSTTRRLFKHDGSTSVPMMAQTKNFNTTEFTPD 240
Db 181 DQLTRLVNLYNALYNGQKNTPEPPIPOSTTRRLFKHDGSTSVPMMAQTKNFNTTEFTPD 240
Qy 241 GHYYDILELPYHGDTLSMPLIAAPYEXKEVPLSALTNTLSAOLI SHWKGNNTRLPRLLPK 300
Db 241 GHYYDILELPYHGDTLSMPLIAAPYEXKEVPLSALTNTLSAOLI SHWKGNNTRLPRLLPK 300
Qy 301 FSLETEVDLKRPLENIGMTDMFRQADFTSLSDQEPPLHYAQALOKVKEVNESGTVASS 360
Db 301 FSLETEVDLKRPLENIGMTDMFRQADFTSLSDQEPPLHYAQALOKVKEVNESGTVASS 360
Qy 361 STAVVSARMAPEETIMDRPFLFVTRHNPCTVLFMGQMEP 402
Db 361 STAVVSARMAPEETIMDRPFLFVTRHNPCTVLFMGQMEP 402
Qy 361 STAVVSARMAPEETIMDRPFLFVTRHNPCTVLFMGQMEP 402
Db 361 STAVVSARMAPEETIMDRPFLFVTRHNPCTVLFMGQMEP 402

RESULT 2
US-08-840-204-2
Sequence 2, Application US/08840204
Patent No. 6103498
GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, STEINGRIMUR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
TITLE OF INVENTION: TYPE 1 (PAI-1) AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSSEE: MORRISON & FOERSTER
CITY: 2000 PENNSYLVANIA AVENUE, NW
STATE: WASHINGTON
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33-949
REFERENCE/DOCKET NUMBER: 30807-20004.00
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-1030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
LENGTH: 402 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein

RESULT 3
US-09-026-408-3
Sequence 3, Application US/09026408
Patent No. 6303338
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
TITLE OF INVENTION: INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEINE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,408
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/934,011
FILING DATE: 15-AUG-1997
PRIOR APPLICATION NUMBER: US 60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEPE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488-0300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-7600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 402 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-026-408-3

Query Match 100.0%; Score 2071; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.6e-204;
 Matches 402; Conservative 0; Indels 0; Gaps 0;

Qy 1 NMSPALTCVLGLALVPGEGSAVHPPSYVAHQASKDRNVFSPY 60
 Db 1 NMSPALTCVLGLALVPGEGSAVHPPSYVAHQASKDRNVFSPY 60

Qy 61 GVASVLMQLQTGGETQQOAAAGFKIDDKGMAPALRHLYKELMGPKDEISITDAI 120
 Db 61 GVASVLMQLQTGGETQQOAAAGFKIDDKGMAPALRHLYKELMGPKDEISITDAI 120

Qy 121 FVORDIKVYQGMMPHEFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMISNLIGKAV 180
 Db 121 FVORDIKVYQGMMPHEFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMISNLIGKAV 180

Qy 181 DQLTRLVNIALYFNGCWTMFSRTRLFLHKSDGSTVSVPMAQTQNKNTYETFTPD 240
 Db 181 DQLTRLVNIALYFNGCWTMFSRTRLFLHKSDGSTVSVPMAQTQNKNTYETFTPD 240

Qy 241 GHYYDILEPLYHGDTLSMFTAAPYEKEVPLSALTINILSASQALISHWKGMNTRLPRLVLPK 300
 Db 241 GHYYDILEPLYHGDTLSMFTAAPYEKEVPLSALTINILSASQALISHWKGMNTRLPRLVLPK 300

Qy 301 FSLETEVDLRKPLENIGMTPDQADFTSLSDQBLPHVAQALKVKIEYNESGTASS 360
 Db 301 FSLETEVDLRKPLENIGMTPDQADFTSLSDQBLPHVAQALKVKIEYNESGTASS 360

Qy 361 STAVIVSARMAPAEELIMDRPFLFVYTRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPAEELIMDRPFLFVYTRHNPTGTVLFMGQVMEP 402

RESULT 5
 US-09-902-684-3
 ; Sequence 3, Application US/09902684
 ; Patent No. 6649738
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/902,684
 ; FILING DATE: 12-Jul-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/026,408
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488-0300002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-902-684-3

Query Match 100.0%; Score 2071; DB 2; Length 402;
 Best Local Similarity 100.0%; Pred. No. 4.6e-204;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NMSPALTCVLGLALVPGEGSAVHPPSYVAHQASKDRNVFSPY 60
 Db 1 NMSPALTCVLGLALVPGEGSAVHPPSYVAHQASKDRNVFSPY 60

Qy 61 GVASVLMQLQTGGETQQOAAAGFKIDDKGMAPALRHLYKELMGPKDEISITDAI 120
 Db 61 GVASVLMQLQTGGETQQOAAAGFKIDDKGMAPALRHLYKELMGPKDEISITDAI 120

Qy 121 FVORDIKVYQGMMPHEFRFLFSTVKQDFSEVERARFIINDWVKTHTKGMISNLIGKAV 180
 Db 1 NMSPALTCVLGLALVPGEGSAVHPPSYVAHQASKDRNVFSPY 60

RESULT 6
US-10-628-395-3
Sequence 3, Application US/10628395
Patent No. 6893970
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR INHIBITOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
STATE: DC
CITY: WASHINGTON
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/628,395
FILING DATE: 29-Jul-2003
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/026,408
FILING DATE: 19-FEB-2001
APPLICATION NUMBER: US/08/934,011
FILING DATE: 15-AUG-1997
APPLICATION NUMBER: US/60/024,056
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEEPE, ERIC K.
REGISTRATION NUMBER: 1488-0300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-628-395-3
Query Match 100.0%; Score 2071; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 4; 6e-204;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 M Q M S P A L T C I V G L A I V F E G S A Y H P P S Y V A H A I S D F C V R V F Q V A Q A S K D R N V F S P Y 60
Db 1 M Q M S P A L T C I V G L A I V F E G S A Y H P P S Y V A H A I S D F C V R V F Q V A Q A S K D R N V F S P Y 60
Qy 1 61 G V A S V L A M I Q M L T G E T Q Q I Q A M G F I K D D K G M A P A L R H L Y K E L M G P M N K D E I S T T D A I 120
Db 1 61 G V A S V L A M I Q M L T G E T Q Q I Q A M G F I K D D K G M A P A L R H L Y K E L M G P M N K D E I S T T D A I 120
Qy 181 D Q L T R L V L V N A L Y F N G Q W K T P F D S S T H R L F H K S D G T S V S P M A Q T K N F Y T E F T T D 240
Db 181 D Q L T R L V L V N A L Y F N G Q W K T P F D S S T H R L F H K S D G T S V S P M A Q T K N F Y T E F T T D 240
Qy 241 G H Y D I L E P Y H G D T L S M F T A A P Y K E V P I S A L T N I S A Q L I S H W K G N N T R L P R I V L P K 300
Db 241 G H Y D I L E P Y H G D T L S M F T A A P Y K E V P I S A L T N I S A Q L I S H W K G N N T R L P R I V L P K 300
Qy 301 F S L E T E V D L R K P L E N G M T D M F R Q A D F T S L S D O E P L H A Q A L Q V K I L E V N E S G T V A S S 360
Db 301 F S L E T E V D L R K P L E N G M T D M F R Q A D F T S L S D O E P L H A Q A L Q V K I L E V N E S G T V A S S 360
Qy 361 S T A V I V S A R M A P E E I I M D R P F L F V R H N P T G V I L E M G Q / N E P 402
Db 361 S T A V I V S A R M A P E E I I M D R P F L F V R H N P T G V I L E M G Q / N E P 402

RESULT 7
US-08-121-714-6
Sequence 6, Application US/08121714
; Patent No. 5470970
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55X
; OPERATING SYSTEM: MS DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,714
; FILING DATE: 09-OCT-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE DOCKET NUMBER: 00530/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEX: 202-371-2600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

APPLICATION NUMBER: 07/938,823
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,296
 FILING DATE: 02/28/91
 APPLICATION NUMBER: 07/662,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 06570/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390
 TYPE: amino acid
 STRANDBEDNESS:
 TOPOLOGY: linear
 US-08-477-108A-6

Query Match 96.9%; Score 2007; DB 1; Length 390;
 Best Local Similarity 99.7%; Pred. No. 1..6..-197;
 Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCVLVGLALVPGESAVHHPSPYAHPLASDFCVRQEVQVAQASKDRNVFSPV 60
 Db 1 MQMSPALTCVLVGLALVPGESAVHHPSPYAHPLASDFCVRQEVQVAQASKDRNVFSPV 60
 Qy 61 GVASYLMLQLQTGGTQQQIQAAMGFKIDDKGMAPALRLYKELMGPMNKDEISTTDAI 120
 Db 61 GVASYLMLQLQTGGTQQQIQAAMGFKIDDKGMAPALRLYKELMGPMNKDEISTTDAI 120
 Qy 121 FVQRDLKLVQGFMPHFFRLFRSTVKQYDFSEVERARFLINDWVKTHTKGMIISNLGKAV 180
 Db 121 FVQRDLKLVQGFMPHFFRLFRSTVKQYDFSEVERARFLINDWVKTHTKGMIISNLGKAV 180
 Qy 181 DQLTRLVLNAYFNGQWKFPPDSSTHRFLHKSDGSTSVPMQACTNKENYTFETTPD 240
 Db 181 DQLTRLVLNAYFNGQWKFPPDSSTHRFLHKSDGSTSVPMQACTNKENYTFETTPD 240
 Qy 241 GHYYDILELPYHGDTLSMFTAAYPEKEVPLSALTNTLSAQIISHWKGNMTRLPRLVLPK 300
 Db 241 GHYYDILELPYHGDTLSMFTAAYPEKEVPLSALTNTLSAQIISHWKGNMTRLPRLVLPK 300
 Qy 301 FSLETEVDLRLKPLENIGMTDMFRQFOADFTSLSDOEPHYAQALQKVIEVNESTVASS 360
 Db 301 FSLETEVDLRLKPLENIGMTDMFRQFOADFTSLSDOEPHYAQALQKVIEVNESTVASS 360
 Qy 361 STAVIVSARMAPEEITMDRPFLEVHNPT 390
 Db 361 STAVIVSARMAPEEITMDRPFLEVHNPT 390

RESULT 8
 Sequence 6, Application US/08477108A
 Patent No. 5801001
 GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 APPLICANT: Zou, Zhiqiang
 APPLICANT: Anticovic, Anthony
 TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2814
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,108A
 FILING DATE: June 7, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/121,714
 FILING DATE: 09/01/93

APPLICATION NUMBER: 07/938,823
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,296
 FILING DATE: 02/28/91
 APPLICATION NUMBER: 07/662,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 06570/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390
 TYPE: amino acid
 STRANDBEDNESS:
 TOPOLOGY: linear
 US-08-477-108A-6

Query Match 95.9%; Score 2007; DB 1; Length 390;
 Best Local Similarity 99.7%; Pred. No. 1..6..-197;
 Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOMSPALTCVLVGLALVPGESAVHHPSPYAHPLASDFCVRQEVQVAQASKDRNVFSPV 60
 Db 1 MQMSPALTCVLVGLALVPGESAVHHPSPYAHPLASDFCVRQEVQVAQASKDRNVFSPV 60
 Qy 61 GVASYLMLQLQTGGTQQQIQAAMGFKIDDKGMAPALRLYKELMGPMNKDEISTTDAI 120
 Db 61 GVASYLMLQLQTGGTQQQIQAAMGFKIDDKGMAPALRLYKELMGPMNKDEISTTDAI 120
 Qy 121 FVQRDLKLVQGFMFFRLFRSTVKQYDFSEVERARFLINDWVKTHTKGMIISNLGKAV 180
 Db 121 FVQRDLKLVQGFMFFRLFRSTVKQYDFSEVERARFLINDWVKTHTKGMIISNLGKAV 180
 Qy 181 DQLTRLVLNAYFNGQWKFPPDSSTHRFLHKSDGSTSVPMQACTNKENYTFETTPD 240
 Db 181 DQLTRLVLNAYFNGQWKFPPDSSTHRFLHKSDGSTSVPMQACTNKENYTFETTPD 240
 Qy 241 GHYYDILELPYHGDTLSMFTAAYPEKEVPLSALTNTLSAQIISHWKGNMTRLPRLVLPK 300
 Db 241 GHYYDILELPYHGDTLSMFTAAYPEKEVPLSALTNTLSAQIISHWKGNMTRLPRLVLPK 300
 Qy 301 FSLETEVDLRLKPLENIGMTDMFRQFOADFTSLSDOEPHYAQALQKVIEVNESTVASS 360
 Db 301 FSLETEVDLRLKPLENIGMTDMFRQFOADFTSLSDOEPHYAQALQKVIEVNESTVASS 360
 Qy 361 STAVIVSARMAPEEITMDRPFLEVHNPT 390
 Db 361 STAVIVSARMAPEEITMDRPFLEVHNPT 390

RESULT 9
 Sequence 6, Application US/08477112
 Patent No. 5905023
 GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 50z or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,108A
 FILING DATE: June 7, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/121,714
 FILING DATE: 09/01/93

COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/477,112
 FILING DATE:
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/121,714
 FILING DATE: 09/01/93
 APPLICATION NUMBER: 07/938,823
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,296
 FILING DATE: 02/28/92
 APPLICATION NUMBER: 07/652,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 06570/002003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: (617) 542-8906
 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 390
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-477-112-6

Query Match 96.9%; Score 2007; DB 1; Length 390;
 Best Local Similarity 99.7%; Pred. No. 1.6e-197;
 Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTIVLGLALVFGGSAVHPSSVYAHLASDFGYRVFOQAQSKDRNVFSSY 60
 Db 1 MQMSPALTIVLGLALVFGGSAVHPSSVYAHLASDFGYRVFOQAQSKDRNVFSSY 60

Qy 61 GVASYLAMQLTTGGBTOOQIQAAGFKIDDKGMAPALRHLYKELMGPNKDE1STTDI 120
 Db 61 GVASYLAMQLTTGGBTOOQIQAAGFKIDDKGMAPALRHLYKELMGPNKDE1STTDI 120

Qy 121 FVQRDLKLWQGMPHFFRLFRSTYKVQDVSSEVERARFLINDWVKTHTKGMSNLGKAV 180
 Db 121 FVQRDLKLWQGMPHFFRLFRSTYKVQDVSSEVERARFLINDWVKTHTKGMSNLGKAV 180

Qy 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240
 Db 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240

Qy 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240
 Db 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240

Qy 241 GHYDILELPYHGDTLSMFIAAPTEKEVPLSALTNLISQIISHWKGNNTRPLLVPK 300
 Db 241 GHYDILELPYHGDTLSMFIAAPTEKEVPLSALTNLISQIISHWKGNNTRPLLVPK 300

Qy 301 FSLETEVDLRKPENGMQTMFROQADFTSLSDOEPLHVAQALQKVKEVNESGTVASS 360
 Db 301 FSLETEVDLRKPENGMQTMFROQADFTSLSDOEPLHVAQALQKVKEVNESGTVASS 360

Qy 361 STAVIVSARMAPEEIMDRFLFYRHNPT 390
 Db 361 STAVIVSARMAPEEIMDRFLFYRHNPT 390

RESULT 10
 PCT-US93-08322-6
 Sequence 6, Application PC/TUSS308322
 GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

RESULT 11
 US-08-840-204-3

ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTY: U.S.A.
 ZIP: 0110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08322
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/938,823
 FILING DATE: 09/01/92
 APPLICATION NUMBER: 07/844,296
 FILING DATE: 02/28/92
 APPLICATION NUMBER: 07/652,216
 FILING DATE: 02/28/91
 ATTORNEY/AGENT INFORMATION:
 NAME: Fraser, Janis K.
 REGISTRATION NUMBER: 34,819
 REFERENCE/DOCKET NUMBER: 00530/072001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEX: (617) 542-8906
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 PCT-US93-08322-6

Query Match 96.9%; Score 2007; DB 4; Length 390;
 Best Local Similarity 99.7%; Pred. No. 1.6e-197;
 Matches 389; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTIVLGLALVFGGSAVHPSSVYAHLASDFGYRVFOQAQSKDRNVFSSY 60
 Db 1 MQMSPALTIVLGLALVFGGSAVHPSSVYAHLASDFGYRVFOQAQSKDRNVFSSY 60

Qy 61 GVASVLANQLTTGGBTOOQIQAAGFKIDDKGMAPALRHLYKELMGPNKDE1STTDI 120
 Db 61 GVASVLANQLTTGGBTOOQIQAAGFKIDDKGMAPALRHLYKELMGPNKDE1STTDI 120

Qy 61 GVASVLANQLTTGGBTOOQIQAAGFKIDDKGMAPALRHLYKELMGPNKDE1STTDI 120
 Db 61 GVASVLANQLTTGGBTOOQIQAAGFKIDDKGMAPALRHLYKELMGPNKDE1STTDI 120

Qy 121 FVQRDLKLWQGMPHFFRLFRSTYKVQDVSSEVERARFLINDWVKTHTKGMSNLGKAV 180
 Db 121 FVQRDLKLWQGMPHFFRLFRSTYKVQDVSSEVERARFLINDWVKTHTKGMSNLGKAV 180

Qy 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240
 Db 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240

Qy 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240
 Db 181 DQLTRVLVLYNLYNGQWTKPDPDSSTHRLFKSDGSIVSPMMAQTNKNTYTFITPD 240

Qy 241 GHYDILELPYHGDTLSMFIAAPTEKEVPLSALTNLISQIISHWKGNNTRPLLVPK 300
 Db 241 GHYDILELPYHGDTLSMFIAAPTEKEVPLSALTNLISQIISHWKGNNTRPLLVPK 300

Qy 301 FSLETEVDLRKPENGMQTMFROQADFTSLSDOEPLHVAQALQKVKEVNESGTVASS 360
 Db 301 FSLETEVDLRKPENGMQTMFROQADFTSLSDOEPLHVAQALQKVKEVNESGTVASS 360

Qy 361 STAVIVSARMAPEEIMDRFLFYRHNPT 390
 Db 361 STAVIVSARMAPEEIMDRFLFYRHNPT 390

RESULT 10
 PCT-US93-08322-6
 Sequence 6, Application PC/TUSS308322
 GENERAL INFORMATION:
 APPLICANT: Sager, Ruth
 TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

Sequence 3, Application US/08840204
Patent No. 6103498
GENERAL INFORMATION:
APPLICANT: LAWRENCE, DANIEL A.
APPLICANT: STEFANSSON, MURKIN MURR P.
TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,204
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 30807-20004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNFDRSWSH
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
LENGTH: 379 amino acids
STRANDEDNESS: single
TOPOLOGY: linear

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RESULT 12
US-09-324-494A-3
; Sequence 3 , Application US/09324494A
; Patent No. 6489143
; GENERAL INFORMATION:
; APPLICANT: STEFANSSON, Steingrimur
; TITLE OF INVENTION: MUTANT PLASMINO
; FILE REFERENCE: 30523/167
; CURRENT APPLICATION NUMBER: US/09/3
; CURRENT FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-324-494A-3

Query Match      94.5% ; Score
Best Local Similarity 10.0% ; Pre
Matches 379; Conservative 0; M
; M
Db    1 VHHPPSXYAHLASDFGIVRVEQQVA
; VHHPPSXYAHLASDFGIVRVEQQVA
Qy    84 AMGFKDDKGMAPALRHLYKELMG
; AMGFKDDKGMAPALRHLYKELMG
Db    61 AMGFKDDKGMAPALRHLYKELMG
; AMGFKDDKGMAPALRHLYKELMG
Db    144 VKQVDFSEVERARFIINDWVKTHI
; VKQVDFSEVERARFIINDWVKTHI
Db    121 VKQVDFSEVERARFIINDWVKTHI
; VKQVDFSEVERARFIINDWVKTHI
Qy    204 DSSTHRLFLFKSDGTSVVPMMAQ
; DSSTHRLFLFKSDGTSVVPMMAQ
Db    181 DSSTHRLFLFKSDGTSVVPMMAQ
; DSSTHRLFLFKSDGTSVVPMMAQ

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Query	Match	94.5%	Score 1958;	DB 2;	Length 379;	
Best Local Matches	Similarity 100.0%;	Pred. No. 1.7e-192;	O; Mismatches 0;	Indels 0;	Gaps 0;	
Qy	24	VHHPPSYVHLASDFGVRYFQOVAQASKDRNVFSPYGVASVLQLTTGGTQQQIA	83	Db	Qy	241 YEKEVPLSALTNIISQQLSHWKGNTRLPKFSLETEVDLKRPLLENLGMTDMFR 300
Db	1	VHHPPSYVHLASDFGVRYFQOVAQASKDRNVFSPYGVASVLQLTTGGTQQQIA	60	Db	324 QFOADFTSLSDQEPLHVAQLQKVIEVNESGTVASSSTAVIVSARMAPPEIIMDRPFLF 383	
Qy	84	AMGFKIDDKGMAPALRHLKELMGPNWKD1STDAIFQDLKLVQGMMPHEFFRLFRST	143	Db	301 QFOADFTSLSDQEPLHVAQLQKVIEVNESGTVASSSTAVIVSARMAPPEIIMDRPFLF 360	
Db	61	AMGFKIDDKGMAPALRHLKELMGPNWKD1STDAIFQDLKLVQGMMPHEFFRLFRST	120	Db	384 VVRHNPNTGTVLFMGQWMEP 402	
Qy	144	VKQDSEVERARFLINDWKRTHTKGMISNLGKGAVDQTRLVNLYFGQWKTTPP	203	Db	361 VVRHNPNTGTVLFMGQWMEP 379	
Db	121	VKQDSEVERARFLINDWKRTHTKGMISNLGKGAVDQTRLVNLYFGQWKTTPP	180		RESULT 13	
Qy	204	DSSTRRLFKSDGSTVSVPMAQTNKFYTEFTPDGHYDILELPYRGDTLSMFIAP	263		US -01-948-997-4	
Db	181	DSSTRRLFKSDGSTVSVPMAQTNKFYTEFTPDGHYDILELPYRGDTLSMFIAP	240		Sequence 4, Application US/08948997	
Qy	264	YEKEVPLSALTNIISQQLSHWKGNTRLPKFSLETEVDLKRPLLENLGMTDMFR	323		Patent No. 6008020	
Db	241	YEKEVPLSALTNIISQQLSHWKGNTRLPKFSLETEVDLKRPLLENLGMTDMFR	300		GENERAL INFORMATION:	
Qy	324	QFOADFTSLSDQEPLHVAQLQKVIEVNESGTVASSSTAVIVSARMAPPEIIMDRPFLF	383		APPLICANT: HASTINGS, GREGG	
Db	301	QFOADFTSLSDQEPLHVAQLQKVIEVNESGTVASSSTAVIVSARMAPPEIIMDRPFLF	360		APPLICANT: COLEMAN, TIM	
Qy	384	VVRHNPNTGTVLFMGQWMEP 402			APPLICANT: LAWRENCE, DANIEL	
Db	361	VVRHNPNTGTVLFMGQWMEP 379			TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF	
					TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR	
					NUMBER OF SEQUENCES: 17	
					CORRESPONDENCE ADDRESS:	
					ADDRESSEE: HUMAN GENOME SCIENCES, INC.	
					STREET: 9410 KEY WEST AVENUE	
					CITY: ROCKVILLE	
					STATE: MD	
					COUNTRY: USA	
					ZIP: 20850	
					COMPUTER READABLE FORM:	
					MEDIUM TYPE: Floppy disk	
					COMPUTER: IBM PC compatible	

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/948,997
 FILING DATE: Oct-10-97
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: A. ANDERS BROOKES
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PF336
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 402 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-948-997-4

Query Match 86.1%; Score 1784; DB 2; Length 402;
 Best Local Similarity 85.3%; Pred. No. 1.e-174;
 Mismatches 30; Indels 0; Gaps 0;
 Matches 343; Conservative 29; Missmatches 30;

Qy 1 MQLSPALTCLVGLALVFGEGSAVHHPSSYVAHLASDFGVRYFQQVAGASKDRNVSFSPY 60
 Db 1 MRMSPVFACTLGLALIPEGGSASYQPOSAAASLATDFGVKFQQVTRBASKDRNVSFSPY 60

Qy 61 GVASVLAMIQLQTGGETQQIQAMGFIDDKGMAPALRHYKELMGPNWKDEISTTDAI 120
 Db 61 GVASVLAMIQLQTGGETQQIQAMFKIEEKGMAPAFLRHYKELMGPNWKDEISTTDAI 120

Qy 121 FVQBDLKLVQGFMMPHFFRLFRSTVQKDSEVERARFLINDWVKTHTKGMSNLGKGAV 180
 Db 121 FVQDLELVHGFMNPFFRLFRSTVQKDSEVERARFLINDWVKTHTKGMSNLGKGAV 180

Qy 181 DQLTRLVNLVNGQWKTTPFDSTRRLFKSDGSTSVPMMAQTNKNTFTTPD 240
 Db 181 DQLTRLVNLVNGQWKTTPFDSTRRLFKSDGSTSVPMMAQTNKNTFTTPD 240

Qy 241 GHYDILELPYHGDTLSMFTAAPYEKEYPLSALTNLISAOQLISHWKGNTNTRPLVLPK 300
 Db 241 GRYDILELPYHGNTLSMFTAAPYEKEYPLSALTNLISAOQLISHWKGNTNTRPLVLPK 300

Qy 301 FSLETEDLRKPFLNGLMTDMFRQOQADFTSLSDQEPLHVAQQLKVIEVNESGTVASS 360
 Db 301 FSLETEDLRKPFLNGLMTDMFRPSQADFSFSDQEFLVSQLQKVIEVNESGTLOSS 360

Qy 361 STAVVSARMAPEEITMDRPLFLVVRNPTGTVLFMGQYMEP 402
 Db 361 STAVVSARMAPEEITMDRPLFLVVRNPTGTVLFMGQYMEP 402

RESULT 15
 US-09-722-292-4

Db 181 DQLTRLVNLVNGQWKTTPFDSTRRLFKSDGSTSVPMMAQTNKNTFTTPD 240
 ; Sequence 4, Application US/09722292
 ; FILE REFERENCE: PF336D1
 ; PATENT NO.: 6541452
 ; GENERAL INFORMATION:
 ; APPLICANT: Hastings et al.
 ; TITLE OF INVENTION: Activator
 ; TITLE OF INVENTION: Activator
 ; CURRENT APPLICATION NUMBER: US/09/722,292
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/348,817
 ; PRIOR FILING DATE: 1999-07-08
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4
 ; LENGTH: 402
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-09-722-292-4

Query Match 86.1%; Score 1784; DB 2; Length 402;
 Best Local Similarity 85.3%; Pred. No. 1.e-174;
 Mismatches 30; Indels 0; Gaps 0;
 Matches 343; Conservative 29; Missmatches 30;

Qy 1 MQLSPALTCLVGLALVFGEGSAVHHPSSYVAHLASDFGVRYFQQVAGASKDRNVSFSPY 60
 Db 1 MRMSPVFACTLGLALIPEGGSASYQPOSAAASLATDFGVKFQQVTRBASKDRNVSFSPY 60

Qy 61 GVASVLAMIQLQTGGETQQIQAMGFIDDKGMAPALRHYKELMGPNWKDEISTTDAI 120
 Db 61 GVASVLAMIQLQTGGETQQIQAMFKIEEKGMAPAFLRHYKELMGPNWKDEISTTDAI 120

SEQ ID NO 4

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Qy 121 FVQRDLKLVQGMPHPFRLPRSTVKQDFSEVERARFINNDWVKHTKGMISNLJGKAV 180
Db 121 FVQRDLVLVAGMPNPFLRFLTRVQDFSEVERARFINNDWVKHTKGMISNLJGKAV 180
Db 181 DQLTRLVLVNALYFNQWKTQFDSSSTHRLFKSDGSTSVPMQAQTNKFNNTYEFITPD 240
Qy 181 DQLTRLVLVNALYFNQWKNPFPESTTHRLFKSDGSTSVPMQAQTNKFNNTYEFITPD 240
Db 181 DQLTRLVLVNALYFNQWKNPFPESTTHRLFKSDGSTSVPMQAQTNKFNNTYEFITPD 240
Qy 241 GHYDYLELPYHGDTLSMELAAPYEKEVPLSALTNLSQLISHWKGNNTRLPRLLVTPK 300
Db 241 GRYDYLELPYHGNTLSMELAAPYEKEVPLSALTSLDAELISOKGNNTRLTRLVLPK 300
Qy 301 FSLETEVDLRKPLENGLMTDMPROADFSLSDOPLHYAQLQKVKEVNESTVASS 360
Db 301 FSLETEVDLRKPLENGLMTDMPROADFSLSDOPLHYAQLQKVKEVNESTVASS 360
Db 361 STAVIVSARMAPEEIIMDRPFLFVRHNPTGTVLFMGOMNEP 402
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Db 361 STALVVSSARMAPEEIIMDRPFLFVRHNPTGTVLFMGOMNEP 402

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Search completed: December 13, 2005, 09:10:56
 Job time : 49 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	402	3 US-09-902-684-3	Sequence 3, Appli
2	2071	100.0	402	4 US-10-060-036-154	Sequence 154, Appli
3	2071	100.0	402	4 US-10-193-656-10	Sequence 10, Appli
4	2071	100.0	402	4 US-10-187-706-6	Sequence 6, Appli
5	2071	100.0	402	4 US-10-170-385-235	Sequence 235, Appli
6	2071	100.0	402	4 US-10-258-609-2	Sequence 2, Appli
7	2071	100.0	402	4 US-10-368-995-4	Sequence 4, Appli
8	2071	100.0	402	4 US-10-197-258-2	Sequence 2, Appli
9	2071	100.0	402	4 US-10-231-9564-420	Sequence 420, Appli
10	2071	100.0	402	4 US-10-628-395-3	Sequence 3, Appli
11	2071	100.0	402	4 US-10-741-600-919	Sequence 919, Appli
12	2071	100.0	402	5 US-10-741-600-920	Sequence 920, Appli
13	2071	100.0	402	5 US-10-832-335A-140	Sequence 140, Appli
14	2071	100.0	402	5 US-10-512-496-6	Sequence 6, Appli
15	2071	100.0	402	5 US-10-505-406-2	Sequence 2, Appli
16	2071	100.0	402	5 US-10-631-467-857	Sequence 420, Appli
17	2071	100.0	402	6 US-11-060-291-8	Sequence 8, Appli
18	1993	96.2	386	4 US-10-368-995-6	Sequence 6, Appli
19	2018	94.5	379	5 US-10-258-609-3	Sequence 3, Appli
20	1958	94.5	379	5 US-10-505-406-3	Sequence 4, Appli
21	1784	86.1	402	3 US-09-957-485-4	Sequence 4, Appli
22	1784	86.1	402	3 US-09-987-021-4	Sequence 4, Appli
23	1784	86.1	402	4 US-10-368-995-2	Sequence 2, Appli
24	1784	86.1	402	4 US-10-355-208-4	Sequence 4, Appli
25	1784	86.1	402	4 US-10-755-891-4	Sequence 4, Appli
26	1746	84.3	400	4 US-10-368-995-8	Sequence 8, Appli
27	1680	81.1	360	4 US-10-037-417-67	Sequence 16, Appli

Qy 1 MQMSPALTCLVGLALVPGEGSAVHPPSYVAHLASDFGYRFOQAQASKDRNVFSFY 60
 Db 1 MQMSPALTCLVGLALVPGESAVHPPSYVAHLASDFGYRFOQAQASKDRNVFSFY 60
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 Db 61 GVASVLAQMLQTTGGTGETQQIQAANGFKIDKGMAPALRHLYKELMGPWKDEI\$TTDAI 120
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 Db 121 FVORDIKLVOGFMPIFFRLFRSTVKQDFSEVERARFINDWKTHTKCMI\$NLGKGV 180
 Qy 181 DQLTRVLVNLAYENGQWIKTPRPDSSTHRLFKSDGSTSVSPMAQTNKFNTEFTTD 240
 Db 181 DQLTRVLVNLAYENGQWIKTPRPDSSTHRLFKSDGSTSVSPMAQTNKFNTEFTTD 240
 Qy 241 GHYDILELPYHGDTLSMFIAAPEYEKEYPLSALTNLSAQI\$HMKGMNTRLPRLVLPK 300
 Db 241 GHYDILELPYHGDTLSMFIAAPEYEKEYPLSALTNLSAQI\$HMKGMNTRLPRLVLPK 300
 Qy 301 FSLETEVDLRKPLENLGMTDMFQOQADFTSLSDQEPHLVAQALQKVKEVNESGTVASS 360
 Db 301 FSLETEVDLRKPLENLGMTDMFQOQADFTSLSDQEPHLVAQALQKVKEVNESGTVASS 360
 Qy 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Qy RESULT 3
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 ; Sequence 10, Application US/10193656
 Qy 241 GHYDILELPYHGDTLSMFIAAPEYEKEYPLSALTNLSAQI\$HMKGMNTRLPRLVLPK 300
 Db 241 GHYDILELPYHGDTLSMFIAAPEYEKEYPLSALTNLSAQI\$HMKGMNTRLPRLVLPK 300
 Qy 301 FSLETEVDLRKPLENLGMTDMFQOQADFTSLSDQEPHLVAQALQKVKEVNESGTVASS 360
 Db 301 FSLETEVDLRKPLENLGMTDMFQOQADFTSLSDQEPHLVAQALQKVKEVNESGTVASS 360
 Qy 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Qy RESULT 2
 Db US-10-060-036-154
 ; Sequence 154, Application US/10060036
 ; Publication No. US20030073144A1
 GENERAL INFORMATION:
 APPLICANT: Benson, Darin R.
 APPLICANT: Kalos, Michael J.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Persing, David H.
 APPLICANT: Repler, William T.
 APPLICANT: Jiang, Yugu
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
 FILE REFERENCE: 210121..566
 CURRENT APPLICATION NUMBER: US/10/066,036
 CURRENT FILING DATE: 2002-01-10
 NUMBER SEQ ID NOS: 4560
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 154
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-060-036-154
 Query Match 100.0%; Score 2071; DB 4; Length 402;
 Best Local Similarity 100.0%; Pred. No. 3e-190; Gaps 0; Gaps 0;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQMSPALTCLVGLALVPGESAVHPPSYVAHLASDFGYRFOQAQASKDRNVFSFY 60
 Db 1 MQMSPALTCLVGLALVPGESAVHPPSYVAHLASDFGYRFOQAQASKDRNVFSFY 60
 Qy 61 GVASVLAQMLQTTGGTGETQQIQAANGFKIDKGMAPALRHLYKELMGPWKDEI\$TTDAI 120
 Db 61 GVASVLAQMLQTTGGTGETQQIQAANGFKIDKGMAPALRHLYKELMGPWKDEI\$TTDAI 120
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 Qy 181 DQLTRVLVNLAYENGQWIKTPRPDSSTHRLFKSDGSTSVSPMAQTNKFNTEFTPD 240
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 Qy 241 GHYDILELPYHGDTLSMFIAAPEYEKEYPLSALTNLSAQI\$HMKGMNTRLPRLVLPK 300
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 Qy 301 FSLETEVDLRKPLENLGMTDMFQOQADFTSLSDQEPHLVAQALQKVKEVNESGTVASS 360
 Db 301 FSLETEVDLRKPLENLGMTDMFQOQADFTSLSDQEPHLVAQALQKVKEVNESGTVASS 360
 Qy 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
 Db 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402

Db 361 STAVIVSARMAPEEIMDRPFLFVTRHNPCTVLPMQVNEP 402

RESULT 4
US-10-128-706-6

Sequence 6, Application US/10128706
Publication No. US20030199463A1

GENERAL INFORMATION:
APPLICANT: IATESCU, SILVIU
TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1

FILE REFERENCE: 0575/66601
CURRENT APPLICATION NUMBER: US/10/128,706

CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 17

SEQ ID NO 6
SOFTWARE: Patentin version 3.1

CURRENT FILING DATE: 2002-04-23
SEQ ID NO 6
TYPE: PRT
ORGANISM: HOMO SAPIENS

US-10-128-706-6
Query Match 100.0%; Score 2071; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVGLALVFGEGSAVHPPSYVAHLASDFGVRVFOQVAQASKDRNVFSPY 60

Db 1 MQMSPALTCLVGLALVFGEGSAVHPPSYVAHLASDFGVRVFOQVAQASKDRNVFSPY 60

Qy 61 GVASVILMLQLQTGGTQQIQAAMGFKIDDKGMAPALRHYKELMGPNKDEISTTDAI 120

Db 61 GVASVILMLQLQTGGTQQIQAAMGFKIDDKGMAPALRHYKELMGPNKDEISTTDAI 120

Qy 61 GVASVILMLQLQTGGTQQIQAAMGFKIDDKGMAPALRHYKELMGPNKDEISTTDAI 120

Db 61 GVASVILMLQLQTGGTQQIQAAMGFKIDDKGMAPALRHYKELMGPNKDEISTTDAI 120

Qy 121 FVQRDLKLVQGFMPFRPLRSTVQVDSEVERARFLINDWVKTHTKGMISNLGKAV 180

Db 121 FVQRDLKLVQGFMPFRPLRSTVQVDSEVERARFLINDWVKTHTKGMISNLGKAV 180

Qy 121 FVQRDLKLVQGFMPFRPLRSTVQVDSEVERARFLINDWVKTHTKGMISNLGKAV 180

Db 121 FVQRDLKLVQGFMPFRPLRSTVQVDSEVERARFLINDWVKTHTKGMISNLGKAV 180

Qy 181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRLFLHKSDGSTVSVPMMAQTNKNEYTEFTPD 240

Db 181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRLFLHKSDGSTVSVPMMAQTNKNEYTEFTPD 240

Qy 181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRLFLHKSDGSTVSVPMMAQTNKNEYTEFTPD 240

Db 181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRLFLHKSDGSTVSVPMMAQTNKNEYTEFTPD 240

Qy 241 GHYDILELPLYHGDTLSMFAAPYKEVPLSALTNLISQLOKVKIEVNEGTASS 360

Db 241 GHYDILELPLYHGDTLSMFAAPYKEVPLSALTNLISQLOKVKIEVNEGTASS 360

Qy 241 GHYDILELPLYHGDTLSMFAAPYKEVPLSALTNLISQLOKVKIEVNEGTASS 360

Db 241 GHYDILELPLYHGDTLSMFAAPYKEVPLSALTNLISQLOKVKIEVNEGTASS 360

Qy 301 FSLETDEVLRKPLENIGMTDMFRQFQADFTSLSDQEPFLHYAQALQVKIEVNEGTASS 360

Db 301 FSLETDEVLRKPLENIGMTDMFRQFQADFTSLSDQEPFLHYAQALQVKIEVNEGTASS 360

Qy 361 STAVIVSARMAPEEIMDRPFLFVTRHNPCTVLPMQVNEP 402

Db 361 STAVIVSARMAPEEIMDRPFLFVTRHNPCTVLPMQVNEP 402

1 MQMSPALTCIVLGLAVFGEGLAVHPPSTVAHLASDFGVRVFOQAASKDRNVVFSPY 60
 Qy 61 GVASVIALMQLTTGGTQQTOQOANGFKIDDKGMAPALRHYKELMGPNKDEI STTDAI 120
 Db 61 GVASVIALMQLTTGGTQQTOQOANGFKIDDKGMAPALRHYKELMGPNKDEI STTDAI 120
 Qy 121 FVORDIKLJVGCFMPHPFLRFLSTVQDSEVERAFINDWKTHTKGMISNLGKAV 180
 Db 121 FVORDIKLJVGCFMPHPFLRFLSTVQDSEVERAFINDWKTHTKGMISNLGKAV 180
 Db 121 DOLTRILVNLNLYNGFQWKKPFDSSTHRFLFKSDGSTSVSPMMAQTNKFNTEFTTPD 240
 Qy 121 DOLTRILVNLNLYNGFQWKKPFDSSTHRFLFKSDGSTSVSPMMAQTNKFNTEFTTPD 240
 Db 121 CHYYDLELPYHGDTLSMFAAYPEKEVPLSALTNLISQTLISHWKGNMTRPLVLPK 300
 Qy 121 GHYYDLELPYHGDTLSMFAAYPEKEVPLSALTNLISQTLISHWKGNMTRPLVLPK 300
 Db 121 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360
 Qy 121 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360
 Db 121 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360
 Qy 121 STAVIVSARMAPEEIMDRPFLVRRHNPCTVLFMGMQMEP 402
 Db 121 STAVIVSARMAPEEIMDRPFLVRRHNPCTVLFMGMQMEP 402
 Qy 121 STAVIVSARMAPEEIMDRPFLVRRHNPCTVLFMGMQMEP 402
 Db 121 STAVIVSARMAPEEIMDRPFLVRRHNPCTVLFMGMQMEP 402

RESULT 7
 US-10-368-995-4
 ; Sequence 4, Application US/10368995
 ; Publication No. US20030217371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vaughan, Douglas E.
 ; ATTORNEY OR AGENT NAME: Mebut
 ; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
 ; TITLE OF INVENTION: ANIMAL
 ; FILE REFERENCE: 1242/43
 ; CURRENT APPLICATION NUMBER: US/10/368,995
 ; CURRENT FILING DATE: 2003-02-19
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 402
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-10-368-995-4

Query Match 100.0%; Score 2071; DB 4; Length 402;
 Best Local Similarity 100.0%; Pred. No. 3e-190; Indels 0; Gaps 0;
 Matches 402; Conservative 0; Missmatches 0;

Qy 1 MQMSPALTCIVLGLAVFGEGLAVHPPSTVAHLASDFGVRVFOQAASKDRNVVFSPY 60
 Db 1 MQMSPALTCIVLGLAVFGEGLAVHPPSTVAHLASDFGVRVFOQAASKDRNVVFSPY 60
 Qy 121 GVASVILMQLTTGGTQQTOQOANGFKIDDKGMAPALRHYKELMGPNKDEI STTDAI 120
 Db 121 GVASVILMQLTTGGTQQTOQOANGFKIDDKGMAPALRHYKELMGPNKDEI STTDAI 120
 Qy 121 FVORDIKLJVGFMFFFLRFLSTVQDSEVERAFINDWKTHTKGMISNLGKAV 180
 Db 121 FVORDIKLJVGFMFFFLRFLSTVQDSEVERAFINDWKTHTKGMISNLGKAV 180
 Qy 121 DOLTRILVNLNLYNGFQWKKPFDSSTHRFLFKSDGSTSVSPMMAQTNKFNTEFTTPD 240
 Db 121 DOLTRILVNLNLYNGFQWKKPFDSSTHRFLFKSDGSTSVSPMMAQTNKFNTEFTTPD 240
 Qy 241 GHYYDLELPYHGDTLSMFAAYPEKEVPLSALTNLISQTLISHWKGNMTRPLVLPK 300
 Db 241 GHYYDLELPYHGDTLSMFAAYPEKEVPLSALTNLISQTLISHWKGNMTRPLVLPK 300
 Qy 301 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360
 Db 301 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360
 Qy 361 STAVIVSARMAPEEIMDRPFLVRRHNPCTVLFMGMQMEP 402
 Db 361 STAVIVSARMAPEEIMDRPFLVRRHNPCTVLFMGMQMEP 402

RESULT 9
 US-10-211-956A-420
 ; Sequence 420, Application US/10231956A
 ; Publication No. US20040053233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lorenz, James B.
 ; ATTORNEY OR AGENT NAME: Weiduan
 ; TITLE OF INVENTION: Bogenberger, Jakob
 ; APPLICANT: Holland, Sacha
 ; APPLICANT: Rigel Pharmaceuticals, Incorporated
 ; TITLE OF INVENTION: Modulators of Angiogenesis
 ; FILE REFERENCE: 021044-004100US

Qy 181 DOLTRILVNLNLYNGFQWKKPFDSSTHRFLFKSDGSTSVSPMMAQTNKFNTEFTTPD 240
 Db 181 DOLTRILVNLNLYNGFQWKKPFDSSTHRFLFKSDGSTSVSPMMAQTNKFNTEFTTPD 240
 Qy 241 GHYYDLELPYHGDTLSMFAAYPEKEVPLSALTNLISQTLISHWKGNMTRPLVLPK 300
 Db 241 GHYYDLELPYHGDTLSMFAAYPEKEVPLSALTNLISQTLISHWKGNMTRPLVLPK 300
 Qy 301 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360
 Db 301 FSLETEVDLRKPENLGMTMFRQADFTSLSDOEPLHYAQALOKVKIEVNESGVASS 360

CURRENT APPLICATION NUMBER: US/10/231,956A
 CURRENT FILING DATE: 2001-08-30
 NUMBER OF SEQ ID NO: 522
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 420
 LENGTH: 402
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-231-956A-420

Query Match 100.0%; Score 2071; DB 4; Length 402;
 Best Local Similarity 100.0%; Pred. No. 3e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQMSPALTCLVGLALVGEESAVHPPSTYIAHLASDEGIVFQVOQAQSKDRNVTFSVY 60
 Db 1 NQMSPALTCLVGLALVGEESAVHPPSTYIAHLASDEGIVFQVOQAQSKDRNVTFSVY 60

Qy 61 GVASVIALMQLQTGGTQQIQAANGFKIDKGMAPALRILYKELMGPWNKDEISTDAI 120
 Db 61 GVASVIALMQLQTGGTQQIQAANGFKIDKGMAPALRILYKELMGPWNKDEISTDAI 120

Qy 121 FVQRDLKLVQGFMMPHFFRLFRSTVKQDFSEVERARFINDWVKHTKGAV 180
 Db 121 FVQRDLKLVQGFMMPHFFRLFRSTVKQDFSEVERARFINDWVKHTKGAV 180

Qy 181 DQLTRLVNLVNLAYENGOWKTFPDSSTTHPLFKSDGSITVSVPMAQTKNFNYTEFTTPD 240
 Db 181 DQLTRLVNLVNLAYENGOWKTFPDSSTTHPLFKSDGSITVSVPMAQTKNFNYTEFTTPD 240

Qy 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNLISQLISHYKGNNTRLPRLLVPK 300
 Db 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNLISQLISHYKGNNTRLPRLLVPK 300

Qy 301 FSLETEVDLRKPLENIGMTDMFRQOFQDFTSLSDQEPLHYAQALQKVIEVNESGTVASS 360
 Db 301 FSLETEVDLRKPLENIGMTDMFRQOFQDFTSLSDQEPLHYAQALQKVIEVNESGTVASS 360

Qy 361 STAVIVSARMAPEEITIMDRPFLFVVRHNPCTVFLFMQVMMEP 402
 Db 361 STAVIVSARMAPEEITIMDRPFLFVVRHNPCTVFLFMQVMMEP 402

RESULT 10
 US-10-628-395-3
 Sequence 3, Application US/10/231,956A-420
 Publication No. US/2004/0086978A1
 GENERAL INFORMATION:
 APPLICANT: Ni et al.
 TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR INHIBITOR

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-1934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/628,395
 FILING DATE: 9-Jul-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/026,408
 FILING DATE: 19-FEB-2001
 APPLICATION NUMBER: US 08/934,011
 FILING DATE: 15-AUG-1997

APPLICATION NUMBER: US 60/024,056
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REFERENCE/DOCKET NUMBER: 35,688
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEX/FAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 402 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-628-395-3

Query Match 100.0%; Score 2071; DB 4;
 Best Local Similarity 100.0%; Pred. No. 3e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 1 MQMSPALTCLVGLALVGEESAVHPPSTYIAHLASDEGIVFQVOQAQSKDRNVTFSVY 60
 Db 1 MQMSPALTCLVGLALVGEESAVHPPSTYIAHLASDEGIVFQVOQAQSKDRNVTFSVY 60

Qy 61 GVASVIALMQLQTGGTQQIQAANGFKIDKGMAPALRILYKELMGPWNKDEISTDAI 120
 Db 61 GVASVIALMQLQTGGTQQIQAANGFKIDKGMAPALRILYKELMGPWNKDEISTDAI 120

Qy 121 FVQRDLKLVQGFMMPHFFRLFRSTVKQDFSEVERARFINDWVKHTKGAV 180
 Db 121 FVQRDLKLVQGFMMPHFFRLFRSTVKQDFSEVERARFINDWVKHTKGAV 180

Qy 181 DQLTRLVNLVNLAYENGOWKTFPDSSTTHPLFKSDGSITVSVPMAQTKNFNYTEFTTPD 240
 Db 181 DQLTRLVNLVNLAYENGOWKTFPDSSTTHPLFKSDGSITVSVPMAQTKNFNYTEFTTPD 240

Qy 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNLISQLISHYKGNNTRLPRLLVPK 300
 Db 241 GHYYDILELPYHGDTLSMFIAPYEKEVPLSALTNLISQLISHYKGNNTRLPRLLVPK 300

Qy 301 FSLETEVDLRKPLENIGMTDMFRQOFQDFTSLSDQEPLHYAQALQKVIEVNESGTVASS 360
 Db 301 FSLETEVDLRKPLENIGMTDMFRQOFQDFTSLSDQEPLHYAQALQKVIEVNESGTVASS 360

RESULT 11
 US-10-741-600-919
 Sequence 919, Application US/10/741600
 Publication No. US/2005/026169A1
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 919
 LENGTH: 402
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-919

Query Match 100.0%; Score 2071; DB 5;
 Best Local Similarity 100.0%; Pred. No. 3e-190;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQMSPALTCLVGLALVYNGPMPHEFFRPLSTVQDVSVAHPPSYVAHLASDFGRVFCQVAQASKDRNVFSY 60
 Db 1 MQMSPALTCLVGLALVYNGPMPHEFFRPLSTVQDVSVAHPPSYVAHLASDFGRVFCQVAQASKDRNVFSY 60
 Qy 61 GVASYLAMLOLTGGTGTGGTQQOIQANGFKIDDKGMAPALRHYKEIIMGPWNKDEI STTDAI 120
 Db 61 GVASYLAMLOLTGGTGTGGTQQOIQANGFKIDDKGMAPALRHYKEIIMGPWNKDEI STTDAI 120
 Qy 121 FVQRDLKLVQGFMPIFFRPLSTVQDVSSEVERARFLINDWVKTHTKGMSNLGKGAV 180
 Db 121 FVQRDLKLVQGFMPIFFRPLSTVQDVSSEVERARFLINDWVKTHTKGMSNLGKGAV 180
 Qy 181 DQLTRLVLYNALYNGQWIKPFPDSTSRRLFHKSDGTSVPMMAQTKNFNTTEFTPD 240
 Db 181 DQLTRLVLYNALYNGQWIKPFPDSTSRRLFHKSDGTSVPMMAQTKNFNTTEFTPD 240
 Qy 241 GHYYDILELPYHGDTLSMFLAAYPKEVPLSALTNLSAOLI SHWKGNNTRLPRLLVPLK 300
 Db 241 GHYYDILELPYHGDTLSMFLAAYPKEVPLSALTNLSAOLI SHWKGNNTRLPRLLVPLK 300
 Qy 301 FSLETEDLKRPLENGMTPMFQADFTSLSDOBPLHVAQALQVKIEVNESTVASS 360
 Db 301 FSLETEDLKRPLENGMTPMFQADFTSLSDOBPLHVAQALQVKIEVNESTVASS 360
 Qy 361 STAVIVSARMAPEEIMDRPFLFVRNPTGTVLFMGQYMEP 402
 Db 361 STAVIVSARMAPEEIMDRPFLFVRNPTGTVLFMGQYMEP 402

RESULT 12
 US-10-741-600-920
 ; Sequence 920, Application US/10741600
 ; Publication No. US2005026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C101499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 920
 ; LENGTH: 402
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-741-600-920

Query Match 100.0%; Score 2071; DB 5; Length 402;
 Best Local Similarity 100.0%; Pred. No. 3e-190;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQMSPALTCLVGLALVYNGPMPHEFFRPLSTVQDVSVAHPPSYVAHLASDFGRVFCQVAQASKDRNVFSY 60
 Db 1 MQMSPALTCLVGLALVYNGPMPHEFFRPLSTVQDVSVAHPPSYVAHLASDFGRVFCQVAQASKDRNVFSY 60
 Qy 61 GVASYLAMLOLTGGTGTGGTQQOIQANGFKIDDKGMAPALRHYKEIIMGPWNKDEI STTDAI 120
 Db 61 GVASYLAMLOLTGGTGTGGTQQOIQANGFKIDDKGMAPALRHYKEIIMGPWNKDEI STTDAI 120
 Qy 121 FVQRDLKLVQGFMPIFFRPLSTVQDVSSEVERARFLINDWVKTHTKGMSNLGKGAV 180
 Db 121 FVQRDLKLVQGFMPIFFRPLSTVQDVSSEVERARFLINDWVKTHTKGMSNLGKGAV 180
 Qy 181 DQLTRLVLYNALYNGQWIKPFPDSTSRRLFHKSDGTSVPMMAQTKNFNTTEFTPD 240
 Db 181 DQLTRLVLYNALYNGQWIKPFPDSTSRRLFHKSDGTSVPMMAQTKNFNTTEFTPD 240
 Qy 241 GHYYDILELPYHGDTLSMFLAAYPKEVPLSALTNLSAOLI SHWKGNNTRLPRLLVPLK 300
 Db 241 GHYYDILELPYHGDTLSMFLAAYPKEVPLSALTNLSAOLI SHWKGNNTRLPRLLVPLK 300
 Qy 301 FSLETEDLKRPLENGMTPMFQADFTSLSDOBPLHVAQALQVKIEVNESTVASS 360
 Db 301 FSLETEDLKRPLENGMTPMFQADFTSLSDOBPLHVAQALQVKIEVNESTVASS 360
 Qy 361 STAVIVSARMAPEEIMDRPFLFVRNPTGTVLFMGQYMEP 402
 Db 361 STAVIVSARMAPEEIMDRPFLFVRNPTGTVLFMGQYMEP 402

RESULT 14
 US-10-512-496-6
 ; Sequence 6, Application US/10512496
 ; Publication No. US20050148527A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ITESCU, SILVIU
 ; TITLE OF INVENTION: A DNA ENZYME TO INHIBIT PLASMINOGEN ACTIVATOR INHIBITOR-1
 ; FILE REFERENCE: 0575/66601-A-PCT-US

RESULT 17
US-11-060-291-8

; Sequence 8, Application US/11050291
; Publication No. US20050186608A1
; GENERAL INFORMATION:
; APPLICANT: Ober, Byron
; TITLE OF INVENTION: A Method for the Production of Transgenic Proteins Usseful in the Treatment of Obesity and Diabetes
; CURRENT APPLICATION NUMBER: US/11/060,291
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/545,750
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-060-291-8

Query Match 100.0%; Score 2071; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 3e-190;
Matches 402; Conservative 0; N mismatches 0;
Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVGLALVGEGSAVHPPSYVAHLASDFCVRFOQVAQASKDRNVSFSY 60
Db 1 MQMSPALTCLVGLALVGEGSAVHPPSYVAHLASDFCVRFOQVAQASKDRNVSFSY 60
Qy 61 GVASVLANMQLTIGETCQQIQAAMGFKDDKGMAPAFLRHYYKELMGPKNDKEISTDAI 120
Db 61 GVASVLANMQLTIGETCQQIQAAMGFKDDKGMAPAFLRHYYKELMGPKNDKEISTDAI 120
Qy 121 FVQRDLKLQGFMHPFRFRSTYKVQDSEVERBARFINDWKTHTKGMISNLGKAV 180
Db 121 FVQRDLKLQGFMHPFRFRSTYKVQDSEVERBARFINDWKTHTKGMISNLGKAV 180
Qy 181 DQLTRVLVNALYFNGQWKTTPFPDSSTHRLFKSDGSTVSPVMAQTNKFNTEFTTPD 240
Db 181 DQLTRVLVNALYFNGQWKTTPFPDSSTHRLFKSDGSTVSPVMAQTNKFNTEFTTPD 240
Qy 241 GHYDILEPYHGDTLSMTAAPEKEYVPSALTNLSQLISHWKGNTRPLLVFK 300
Db 241 GHYDILEPYHGDTLSMTAAPEKEYVPSALTNLSQLISHWKGNTRPLLVFK 300
Qy 301 FSLETEVDLRKPLENLGMDFRQADFTSLSOEPFLVIAQLOVKVKEVNESGTVASS 360
Db 301 FSLETEVDLRKPLENLGMDFRQADFTSLSOEPFLVIAQLOVKVKEVNESGTVASS 360
Qy 361 STAVIVSARMAPEETIMDRPFLFVVRNPTGTVLFMGQMEP 402
Db 361 STAVIVSARMAPEETIMDRPFLFVVRNPTGTVLFMGQMEP 402

RESULT 18
US-9-0-995-6

; Sequence 6, Application US/10368995
; Publication No. US20030217371A1

; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; APPLICANT: Eren, Mesut
; APPLICANT: Declerk, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON ANIMAL
; TITLE OF INVENTION: ANIMAL
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 6
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Human
US-10-368-995-6

Query Match 96.2%; Score 1993; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 9e-183;
Matches 386; Conservative 0; N mismatches 0;
Indels 0; Gaps 0;

Qy 17 VFGEGSAVHPPSYVAHLASDFCVRFOQVAQASKDRNVSFSYGVASVLMQLTTCGE 76
Db 1 VFGEGSAVHPPSYVAHLASDFCVRFOQVAQASKDRNVSFSYGVASVLMQLTTCGE 60

Qy 77 TQQQIAAMGFKDDKGMAPAFLRHYYKELMGPKNDKEISTDAI FVORDLKLVQGFMPHF 136
Db 61 TQQQIAAMGFKDDKGMAPAFLRHYYKELMGPKNDKEISTDAI FVORDLKLVQGFMPHF 120

Qy 137 FRFRSTYKVQDSEVERBARFINDWKTHTKGMISNLGKAVDQLTRLYNALYFNG 196
Db 121 FRFRSTYKVQDSEVERBARFINDWKTHTKGMISNLGKAVDQLTRLYNALYFNG 180

Qy 197 QWKTTPFPDSSTHRLFKSDGSTVSPVMAQTNKFNTEFTPDGHYDILEPYHGDTL 256
Db 181 QWKTTPFPDSSTHRLFKSDGSTVSPVMAQTNKFNTEFTPDGHYDILEPYHGDTL 240

Qy 257 SMFTAYPEKEYVPLSATNLSQLISHWKGNTRPLLVLPKPSLETEVDLRKPLENL 316
Db 241 SMFTAYPEKEYVPLSATNLSQLISHWKGNTRPLLVLPKPSLETEVDLRKPLENL 300

Qy 317 GMDDMFRQFQADFTSLSOEPFLHVAQLOVKVKEVNESGTVASSSTAVVSARMAPBII 376
Db 301 GMDDMFRQFQADFTSLSOEPFLHVAQLOVKVKEVNESGTVASSSTAVVSARMAPBII 360

Qy 377 MDRPFPLFVVRNPTGTVLFMGQMEP 402
Db 361 MDRPFPLFVVRNPTGTVLFMGQMEP 386

RESULT 19
US-10-259-603-3

; Sequence 3, Application US/10259609
; Publication No. US20030216321A1
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Daniel A.
; APPLICANT: SPEARANSON, Steinimir P.
; TITLE OF INVENTION: MUTANT PLASMIDGEN ACTIVATOR - INHIBITOR TYPE 1 (PAI-1) AND USES THEREOF
; FILE REFERENCE: 3023/167
; CURRENT APPLICATION NUMBER: US/10/259,609
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/324,494A
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 3
; LENGTH: 379
; SOFTWARE: PatentIn version 3.1
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-259-603-3

Query Match 94.5%; Score 1958; DB 4; Length 379;
Best Local Similarity 100.0%; Pred. No. 2e-179;

Matches	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
24	VHPPSYYAHLASDFGVRYFQQVQAQSKDRNTYFSPYGVASVLAMQLTGTGETQQIQA	83						
1	VHPPSYYAHLASDFGVRFQVQAQSKDRNVFSPYGVASVLAMQLTGTGETQQIQA	60						
84	AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTDAIFQDILKLVQGMPHFFPLFRST	143						
61	AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTDAIFQDILKLVQGMPHFFPLFRST	120						
144	VHQYDFSEVERARFLINNDWKHTKGMTSLNIGKAVDQLTRLVNLVLYENQWQKTPFP	203						
121	VHQYDFSEVERARFLINNDWKHTKGMTSLNIGKAVDQLTRLVNLVLYENQWQKTPFP	180						
204	DSSTHRRLFHKSOGSTIVSPMMAQTQNKENYTESTPDGHYDILEPQHGDLSMFIAP	263						
181	DSSTHRRLFHKSOGSTIVSPMMAQTQNKENYTESTPDGHYDILEPQHGDLSMFIAP	240						
241	YEKEVPLSALTNTLISQLISHWKGNMTRPLPKSLETEVDLRKPLENLGMTDMPF	323						
241	YEKEVPLSALTNTLISQLISHWKGNMTRPLPKSLETEVDLRKPLENLGMTDMPF	300						
324	QFOADFTSLSDQEPHLVQALOKVIEYNESGTYASSSTAVIVSARMAPEEIMDRPFLF	383						
301	QFOADFTSLSDQEPHLVQALOKVIEYNESGTYASSSTAVIVSARMAPEEIMDRPFLF	360						
264	YEKEVPLSALTNTLISQLISHWKGNMTRPLPKSLETEVDLRKPLENLGMTDMPF	323						
241	YEKEVPLSALTNTLISQLISHWKGNMTRPLPKSLETEVDLRKPLENLGMTDMPF	300						
324	QFOADFTSLSDQEPHLVQALOKVIEYNESGTYASSSTAVIVSARMAPEEIMDRPFLF	383						
301	QFOADFTSLSDQEPHLVQALOKVIEYNESGTYASSSTAVIVSARMAPEEIMDRPFLF	360						
204	VVRHNPPTGTVLFNGQMEP	402						
181	VVRHNPPTGTVLFNGQMEP	400						
264	YEKEVPLSALTNTLISQLISHWKGNMTRPLPKSLETEVDLRKPLENLGMTDMPF	323						
241	YEKEVPLSALTNTLISQLISHWKGNMTRPLPKSLETEVDLRKPLENLGMTDMPF	300						
324	QFOADFTSLSDQEPHLVQALOKVIEYNESGTYASSSTAVIVSARMAPEEIMDRPFLF	383						
301	QFOADFTSLSDQEPHLVQALOKVIEYNESGTYASSSTAVIVSARMAPEEIMDRPFLF	360						
204	VVRHNPPTGTVLFNGQMEP	402						
181	VVRHNPPTGTVLFNGQMEP	379						
RESULT 21								
		US-09-957-485-4						
		; Sequence 4, Application US/09957485						
		; Patent No. US2002014165A1						
		; GENERAL INFORMATION:						
		; APPLICANT: Human Genome Sciences, Inc. et al.						
		; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen						
		; TITLE OF INVENTION: Activator						
		; FILE REFERENCE: PF336P1						
		; CURRENT APPLICATION NUMBER: US/09/957,485						
		; CURRENT FILING DATE: 2001-09-21						
		; PRIORITY NUMBER: US 09/521,664						
		; PRIOR FILING DATE: 2000-03-08						
		; PRIOR APPLICATION NUMBER: US 00/123,704						
		; PRIOR FILING DATE: 1999-03-10						
		; NUMBER OF SEQ ID NOS: 21						
		; SOFTWARE: PatentIn Ver. 2.1						
		; SEQ ID NO 4						
		; LENGTH: 402						
		; TYPE: PRT						
		; ORGANISM: Bos taurus						
		US-09-957-485-4						
Query Match								
		86.1%						
		Score 1784; DB 3; Length 402;						
		Best Local Similarity 85.3%; Pred. No. 1.2e-162;						
		Matches 343; Conservative 29; Mismatches 30; Indels 0; Gaps 0						
		SEQ ID NO 4						
		TYPE: PRT						
		ORGANISM: Bos taurus						
RESULT 20								
		US-10-506-406-3						
		; Sequence 3, Application US/10506406						
		; Publication No. US20050158295A1						
		; GENERAL INFORMATION:						
		; APPLICANT: Swiercz, Rafal						
		; APPLICANT: Salman, Steven						
		; APPLICANT: Jankun, Jerry						
		; APPLICANT: Chorostowska-Wynimko, Joanna						
		; APPLICANT: Skrzypczak-Jankun, Ewa						
		; TITLE OF INVENTION: MODIFIED PLASMINOGEN ACTIVATOR INHIBITOR						
		; TITLE OF INVENTION: TYPE-1 AND METHODS BASED THEREON						
		; FILE REFERENCE: 9471-011-999						
		; CURRENT APPLICATION NUMBER: US/10/506,406						
		; CURRENT FILING DATE: 2004-09-01						
		; PRIORITY NUMBER: PCT/US03/06679						
		; PRIOR FILING DATE: 2003-03-04						
		; PRIOR APPLICATION NUMBER: 60/361,670						
		; PRIOR FILING DATE: 2002-03-04						
		; NUMBER OF SEQ ID NOS: 3						
		; SOFTWARE: FastSEQ for Windows Version 4.0						
		; SEQ ID NO 3						
		; LENGTH: 379						
		; TYPE: PRT						
		; ORGANISM: Homo sapiens						
		; FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						
		TYPE: PRT						
		ORGANISM: Homo sapiens						
		FEATURE: human PAI-1 mature amino acid sequence						
		US-10-506-406-3						
		Query Match						
		94.5%						
		Score 1958; DB 5; Length 379;						
		Best Local Similarity 100.0%; Pred. No. 2e-179;						
		Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
		SEQ ID NO 3						

Db 361 STALVVSSARMAPEETIMDRPFLFVYRHNPTGTVLFMGQVMEP 402

RESULT 22
US-09-987-021-4
; Sequence 4, Application US/0987021
; Patent No. US20030165147A1
; GENERAL INFORMATION:
; APPLICANT: Yepes, et al.
; TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator
; FILE REFERENCE: PF336P2
; CURRENT APPLICATION NUMBER: US/09/987,021
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/557,485
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 09/722,292
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/521,664
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 09/348,817
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/123,704
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 08/348,997
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/028,117
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 4
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-987-021-4

; Publication No. US20030217371A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Douglas E.
; BREN, Mesut
; APPLICANT: Decker, Paul J.
; TITLE OF INVENTION: THERAPEUTIC METHODS EMPLOYING PAI-1 INHIBITORS AND TRANSGENIC NON
; FILE REFERENCE: 1242/43
; CURRENT APPLICATION NUMBER: US/10/368,995
; CURRENT FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Cow
US-10-368-995-2

Query Match 86.1%; Score 1784; DB 4; Length 402;
Best Local Similarity 85.3%; Pred: No. 1.2e-162; Indels 0; Gaps 0;
Matches 343; Conservative 29; Mismatches 30; Indels 0; Gaps 0;

Qy 1 M0MSPALTCLVGLALVGEGSAYHPPSVAHLASDFGVRFQQVAQASKDKRNVFSPY 60
Db 1 MRMSPVFACTALGLALIFGEGSASYQPOSAAASLATDGFVKFQVVRASKDKRNVFSPY 60

Qy 61 GVAVLAMQLTGGTETQQIQAANGFKIDDKGMAPAHLKELMGPNKDESTDAI 120
Db 61 GVAVLAMQLTGGTETQQIQAAMQFKEEKGMAPAFRLYKELMGPNKDESTDAI 120

Qy 121 FVQDLKLVQGFMPHEFFRLFRSTVKQVDSEVERARFLINDWVTKHTKGMISNLGKGRV 180
Db 121 FVQDLKLVQGFMPHEFFRLFRSTVKQVDSEVERARFLINDWVTKHTKGMISNLGKGRV 180

Qy 181 DQLTRLVNLYNFGDKTPFDSSTHRLFFHKSDGSTVSVPMMQACTNKFNTEFTPD 240
Db 181 DQLTRLVNLYNFGDKTPFBSNTHRLFFHKSDGSTVSVPMMQACTNKFNTEFTPD 240

Qy 241 GHYDILELPKHDPLSMLIAAYEKEYPLSAUTLNLQKPLISHWKGMNTRLPBLVLPK 300
Db 241 GRYDILELPHGNTLSMLIAAYEKEYPLSAUTLDAELSQWKGMNTRLPBLVLPK 300

Qy 301 FSLETEVDLRKPLENLGMDFQFQADFTSLSDQEPHLVAQLOVKIEVNESGTASS 360
Db 301 FSLETEVDLRKPLENLGMDFQFQADFTSLSDQEPHLVAQLOVKIEVNESGTASS 360

Qy 361 STAVIVSARMAPEEIMDRPFLFVVRHNPFTGTVLFMGQVMEP 402
Db 361 STAVIVSARMAPEEIMDRPFLFVVRHNPFTGTVLFMGQVMEP 402

Search completed: December 13, 2005, 15:53:12
Job time : 172 secs

RESULT 23
US-10-368-995-2
; Sequence 2, Application US/10368995

Result No.	Score	Query	Match	Length	DB ID	Description
1	2071	100.0	402	6	US-10-821-234-1581	Sequence 1581, App1
2	761	36.7	398	6	US-10-821-234-1488	Sequence 1488, App
3	761	36.7	398	7	US-11-186-284-1985	Sequence 185, App
4	461	22.3	423	6	US-10-821-234-900	Sequence 900, App
5	441	21.3	391	6	US-10-623-155-110	Sequence 110, App
6	440	21.2	425	7	US-11-096-276-2	Sequence 2, App1
7	438.5	21.2	400	6	US-10-623-155-112	Sequence 112, App
8	436.5	21.1	417	7	US-11-147-047-39	Sequence 39, App1
9	398.5	19.2	444	7	US-11-147-047-39	Sequence 1, App1
10	398.5	19.0	444	6	US-10-134-826A-498	Sequence 498, App
11	312	15.1	500	6	US-10-821-234-1458	Sequence 1458, App
12	308.5	14.9	418	7	US-11-186-284-187	Sequence 187, App
13	305	14.7	418	6	US-10-821-234-1331	Sequence 1331, App
14	304	14.7	418	7	US-11-077-716-2	Sequence 2, App1
15	219	10.6	362	7	US-11-010-874-18	Sequence 18, App1
16	202.5	9.8	366	6	US-10-216-245A-2	Sequence 2, App1
17	92.5	4.5	347	6	US-10-793-626-3326	Sequence 3326, App
18	87.5	4.2	530	6	US-10-131-826A-130	Sequence 130, App
19	87	4.2	1034	6	US-10-392-34A-30	Sequence 30, App1
20	86	4.2	484	6	US-10-793-626-2498	Sequence 2498, App
21	96	4.2	1065	6	US-10-793-626-1212	Sequence 1212, App
22	83.5	4.0	448	6	US-10-793-626-1728	Sequence 1728, App
23	81.5	3.9	717	6	US-10-793-626-3022	Sequence 3022, App
24	81.5	3.9	952	6	US-10-821-234-1557	Sequence 1557, App
25	81.5	3.9	952	7	US-11-057-058-54	Sequence 54, App1

RESULT 2

Db 301 FSLETEVDLXPKPLENLGMFTDMFRQFOADFTSLSDOEPLHYAQALQKVKEVNESGTVAASS 360
 Qy 361 STAVIVSARMAPEEITIMDRPFLFVYRHNPTGTVLFMGOQMEP 402
 Db 361 STAVIVSARMAPEEITIMDRPFLFVYRHNPTGTVLFMGOQMEP 402

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmati, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pt_seq_genes Version 1.0

SEQ ID NO: 1486

LENGTH: 398

TYPE: PRT

ORGANISM: Homo sapiens

US-10-821-234-1488

Query Match 36.7%; Score 761; DB 6; Length 398;
 Best Local Similarity 41.3%; Pred. No. 3.5e-61;
 Matches 157; Conservative 77; Mismatches 142; Indels 4; Gaps 3;

Query 25 HHPPSYVAHLASDFGVYFQQVAQSKDRNIVFSPYGVASVLAMQLQTGGTETQQIQA 84
 Db 21 HFNPNSLELGNSNTGQVFNQIVSKRPHNDIVISPHGIASVLGMQLGADGRTKQLAMV 80

Query 85 MGFKIDDKGKAPALRHLXKLLMGPNKDELTSTDIAIFQDQLKLVQGFMPHFFRLFRSTV 144
 Db 81 MRYGYN--GVGKILKKINAKIAVSKKNDIIVTVAANVFVNKAASEIEVPFTYTRNKGDFQCEV 138

Query 145 KQVDSEVERARFLINDWVTHTKSGMSIHLGKGRADV-QLTRLVNLALYFGNGWKTTP 203
 Db 139 RNVNFEDPACDSINAWQNETRMDNIJLSPDLIDGVLTRLVNAVYFKGJWKSREIQ 198

Query 204 DSSTHRRLPKSDESTSVSPMMQATNKENKNYTEFTPDGHYYDLELPYHDTLSMFIAPP 263
 Db 199 PENTKRTFVAADGSKYQVPMQLAQSVFRCSTSAPDLYWNFTELPYGESESISMLAIP 258

Query 264 YEKEVPLSALTNIISQLISHWKGMTRPLPKFSLTEVDLKRPLENLGTMDFR 323
 Db 259 TESSTPLSAIIPHISTKTDSSWMSIMPVKRVQVILPKFAVQDYLKEPLKGITDMD 318

Query 324 QFDQDFTSL-SDQEPLHYAQALQKVIBYNESGTASSSTAVTYSARMAPEEETIMDRPPL 382
 Db 319 SSKANFAKITGTSNLHVSHILQKAKIEVSEDGTKASAATTAILIARSSPPWFTVDRPPL 378

Query 383 FVVRHNPTGTVLFMGOQMEP 402
 Db 379 FFIRENPTGAVLFMGOQINKP 398

RESULT 4

US-10-821-234-900
 Sequence 900, Application US/10821234
 GENERAL INFORMATION:
 APPLICANT: Labat, Ivan
 APPLICANT: Stache-Crain, Birgit
 APPLICANT: Andarmati, Susan
 APPLICANT: Tang, Y. Tom
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

GENERAL INFORMATION:
 APPLICANT: Berger, Allison
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Guillemette, Tracy L.
 APPLICANT: Kamatkar, Shubhangi

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 1704
 SOFTWARE: pt_seq_genes Version 1.0
 SEQ ID NO 900
 LENGTH: 423
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-821-234-900

Query Match 22.3%; Score 461; DB 6; Length 423;
 Best Local Similarity 28.8%; Pred. No. 3..4e-34;
 Matches 119; Conservative 76; Indels 56; Gaps 9;

Qy 38 FGVRVFOQQVAQASKDORNVVFSPYGVASVLAMLOLTGGTQQTOAAMGP----- 87
 Db 19 FALNLFKHLARASPTONFLSPWISSTIMAVYMGSRGSTDQMAKVLPQNEVGANAVTP 78
 Qy 88 -----KIDDKGMAP-----
 Db 79 MTPENPTSGFMQOIQKGSSYDAILQQAADKIHSFRASSAINASTGNLLESVNKL 138
 Qy 122 VORDLKLUVGFMMPHFFRFLFRSTVKQVDSE-VERARFIINDWVKRHTKGMISNLIGKAV 180
 Db 139 GEKSASPRETRILCOKYSSPEAQDLECAEARKKIVSWKTQTKGPKNLPEGSV 198

Qy 181 DOLTRLYVNAFLNGCOWKTPFDGSSTTHRLFKHSDGTVSPVMAQTQKFNYTEFTTPD 240
 Db 199 DGDTRMVLVNAVYFGKWTPEKKLNGLYPERVSAQRTPVQMMYLREKUNI----- 251

Qy 241 GHYYD---IIELPYHCDTLSMFIAPYE--KEVPLSALTNLSQLISHW-KGMNTR 291
 Db 252 GYEDLKAQILELPYAGD-VSMFLLLPDEIADVSTGEELLESEITYDKLNKWTSKDGMAE 310

Qy 292 LPRLLVLPKFSLDETEYDLRKPLENLGMTDMRQFOADFSLTSQDQEPLHVAALQKVIEV 351
 Db 311 DEVEVITPQFKEEYLRSIILRSMGMEDATKGRANSGMSERNLFLSEVHQAMVDV 370

Qy 352 NESGTVAASSSTAVIVSARM-APEEITMDRPFLEVTRHNPCTVLFMGQYMEP 402
 Db 371 NEEGTEAAAGTCGVMTRTGHPGPQFVADHPPFLIMHKITNCILPFGFSSP 423

RESULT 6
 US-10-096-276-2
 Sequence 2, Application US/11096276
 Publication No. US20050260726A1
 GENERAL INFORMATION:
 APPLICANT: Hu, YI
 APPLICANT: Nepomichy, Boris
 APPLICANT: Wale, D. Wade
 TITLE OF INVENTION: Novel Human Protease Inhibitor and Polynucleotides Encoding the Same
 FILE REFERENCE: LEX-0283-USA
 CURRENT APPLICATION NUMBER: US/11/096_276
 CURRENT FILING DATE: 2005-03-31
 PRIOR APPLICATION NUMBER: US/10/419_277
 PRIOR FILING DATE: 2003-04-17
 PRIOR APPLICATION NUMBER: US/10/024_427
 PRIOR FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: US 60/256,287
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEO ID: NO 2
 LENGTH: 425
 TYPE: PRT
 ORGANISM: homo sapiens
 US-11-096-276-2

Query Match 21.2%; Score 440; DB 7; Length 425;
 Best Local Similarity 26.2%; Pred. No. 2.6e-32;
 Matches 111; Conservative 89; Mismatches 149; Indels 74; Gaps 10;

Qy 42 VFOQVQASKDORNVVFSPYGVASVLAMLOLTGGTQQTOAAMGF---KIDDKGMAPA 97
 Db 15 LFQEIGKDDRHKNFSPLSUSAALGMRVLRGARSOSAHQDEVLHNFEPSQNEKSPDPC 74

Qy 98 LRHLYKLM-----
 Db 117 TDAFWYDQLKLVQGMMPHFFRFLRSTVKQVDFSE-VERARFIINDWVKRHTKGMISNL 175

Qy 135 ANRLYGBEQFPICQYEYLDGVQFYHTIESDFQRKPEKSROEINFWECQSOKLKELF 194

Db 176 GKGAQDQLTRVLVNAFLNGCOWKTPFDGSSTTHRLFKHSDGTVSPVMAQTQKFNYTEFT 235
 Db 195 SKDADINASTVLYVNAVYFKRWEYED-----HE--NTVDAFPCLNANEKNSNL 175

Qy 236 FTTPDGHY-----YDILELPYHCDTLSMFIAPYEKEYPLSALTNI--LSAQULIS 283
 Db 243 MNTQKGGLYRIGFTEVKAQILEMRYTKGKLSMFLPSHSDNLKGDEELERKITTYRMV 302

RESULT 5
 US-10-623-155-110
 Sequence 110, Application US/10623155
 Publication No. US20050261166A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Tongtong
 APPLICANT: Peckham, David W.
 APPLICANT: Better, Marc W.
 APPLICANT: Ranger, Gary R.
 APPLICANT: And Diagnosis Of Lung Cancer
 TITLE OF INVENTION: Compositions And Methods For The Therapy
 CURRENT APPLICATION NUMBER: 2003-07-17
 NUMBER OF SEQ ID NOS: 560
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 110
 LENGTH: 391
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-623-155-110

Query Match 21.3%; Score 441; DB 6; Length 391;
 Best Local Similarity 27.4%; Pred. No. 1.9e-32;
 Matches 107; Conservative 92; Indels 165; Gaps 8;

Qy 34 LASPFGVVFQVQAQSDFDRNVFSPYGVASVLAMLOLTGGTQQQQ-----AA 84
 Db 7 VSTRLGFLPKEL-KKTDGNIFSPVQVILTAIGMVLTGTRGATASQEVFHSEKTS 65
 Qy 85 MGFKIDDKGMAPALRHYK-----EIMGPWNKDEIISTTDAFLVQDRLKLVQGFMPPF 137

Qy 284 HWKG--NMTRLPLRLLVLPKFSLETEVDLRKPLENLGTMDFQADFTSLSDQEPFLHYA 341
Db 303 AWSSSENMSSESVVLSFPRRTLEDYDLNSTLQDGITDDETRADLGTVSPBNLYS 362
Qy 342 QALQRKIEVEESGVASSSTAVIYSARMAP--ELIMDRPFLFVNRNPTGTULFMGY 399
Db 363 KIIHCTFVEVDENGTQAAGTAVGAYSERSLRSWVFENANHPFLFTRANKTOTILFYGRY 422

RESULT 7
US-10-623-155-112
Sequence 112, Application US/10623155
Publication No. US20030261166A1

GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peicham, David W.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; CURRENT APPLICATION NUMBER: 210121.45620
; CURRENT FILING DATE: 2003-07-17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 112
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-623-155-112

Query Match 21.2%; Score 438.5; DB 6; Length 400;
Best Local Similarity 27.1%; Pred. No. 3.3e-32;
Matches 108; Conservative 91; Nismatches 165; Indels 35; Gaps 8;

Qy 34 LASDFGVRVQQVAQSKDRNVFSPYGVASVAMLQLTTGGETOOIQ----- 82
Db 7 VSTRUGFDLPEL-KKTNODNINIFFSPVGLTAIGNVLLGTRGATASQLEVFHSEKETKS 65
Qy 83 -----AAMGFKIDD-KSMAPALRHLYKELMGPKWNKDEISTDAIFYORDLKL 128
Db 66 SRIKABEKKVRIAKEGKEENTAEHQOKFELTISKLTDNLNTNLRFGEKTYLF 125
Qy 129 VQGMMPHFPLRFLRSTVKQDF-SEVERARFLINDWVTKHTKGMTISNLKGAVDOLTRLY 187
Db 126 LQKVLDYVEKYHASLQEVDFNAADESKRKINSVVESTCNKIKDLPFGDSLSSSTKLV 185
Qy 188 LVNALYFNGOKWTPPPDSSTHRRLPHKSDGSTSVPMMAOTNKPYTEFTPDHYDIL 247
Db 186 LVNMVYFKQWDREKKKNTKEEKWWNNKTSKSYQMMTQSFS---FTFLEDQAKIL 242
Qy 248 ELPYHGDTLMSMFIAPYKEVPLSALTNTLSAQJLISHW--KGMNTRLPLRLLVLPKFSLFT 305
Db 243 GIPYKNDLNFMLVFLPNID-GLEKIIDKISPEKLVEWTSPGHNEERKVNHLHFRFEVD 301
Qy 306 EVDLRKPLENLGTMDFQADFTSLSDQEPFLFVNRNPTGTULFMGYMEP 402
Db 302 SYDLEAVLJAAMGMGDAFSKADSGMSSGSGLYAQKFHSSFYAVTEGTEAAATGIG 361

Qy 366 VSARM--BEIMDRPFLFVNRNPTGTULFMGYMEP 402
Db 362 FTVTISAPGHENVHCNHPFLFIRHNENSNLLFGFRFSSP 400

RESULT 8
US-11-147-047-39
Sequence 39, Application US/11147047
Publication No. US20030260668A1

; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj R.
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US03/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,197
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; SOFTWARE: FastSEQ for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-147-047-39

Query Match 21.1%; Score 436.5; DB 7; Length 417;
Best Local Similarity 28.7%; Pred. No. 5.3e-32;
Matches 111; Conservative 86; Nismatches 165; Indels 23; Gaps 9;

Qy 27 PPSYVHLASDFGYRVFOOQAQSKDRNVFSPYGVASVAMLQLTTGGETOOIQAMG 86
Db 40 PASQVYSINTDFAFRLYRLVLETPSQNIFSPVSVSTSLAMISLGAHSVTKTQIQLQG 99
Qy 87 FKI--DDKGMAPALRHLYKELMGPKWNKDEISTDAIFYORDLKLQGMPHFRLFIRST 143
Db 100 FNLTTHTPBIAHQFQHLSLTVPSKDLTKNGSAFVKELQDQANFLGNVKRLYAE 159
Qy 144 VKQVDFSEVERARFLINDWVTKHTKGMTISNLKGAVDOLTRLYVNLALYFNGQWTQKTPPP 203
Db 160 VFSTDFNSPIAQRARINSHVVKETQKVYDII--QGDLLTAMVNHIFPKAKWEKFH 217
Qy 204 DSSTHRL-FHKSDGSTVSVPMAQTQNKENY--TEFTTPDGHYYDILBLPYHDGTLMNF 259
Db 218 PEYTRKNPFPLVGEQVTTHVPMHHQKEOFAFGYDTELNC----FVLOMDYKGDAVAPP 271
Qy 260 IAAPYKEVPLSALTNTLSAQJLISHWKGNNTRLPLRLLVLPKFSLFTDLRKPLENLGNT 319
Db 272 VLPRKGK--MRQLEQASARTIRKWSHSLQKRWIEVPIPRFISASYNLETLPKOMIQ 328
Qy 320 DMFRQFQADFTSLSDQEPFLHQAOLQKVKIEVNESGT-VASSSTAVIYSARMAPE-EI 375
Db 329 NVFPK-NADQSKAKRDSLQSVATHKAVLDYSEGGTBATAUTTKEYVRSKDGSYFRTV 387
Qy 376 IMDRPFLFVVRHNPTGTULFMGYMEP 402
Db 388 SFNRTPLMMITNKATDG1FLGRVNP 414

RESULT 9
US-11-071580-1
Sequence 1, Application US/11071580
Publication No. US20050260708A1
GENERAL INFORMATION:
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: LAL, Preeti

APPLICANT: BAUGHN, Mariah R.
 APPLICANT: AZIMZAI, Yalda
 APPLICANT: LU, Duying Aina M.
 APPLICANT: YANG, Junning
 TITLE OF INVENTION: PROTEASES AND PROTEASE INHIBITORS
 FILE REFERENCE: PF-0172 PCT
 CURRENT APPLICATION NUMBER: US/11/071,580
 CURRENT FILING DATE: 2005-03-04
 PRIOR APPLICATION NUMBER: 60/147,986
 PRIOR FILING DATE: 1999-08-09
 PRIOR APPLICATION NUMBER: 60/160,807
 PRIOR FILING DATE: 1999-10-21
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PERL Program
 SEQ ID NO: 1
 LENGTH: 444
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No: 088718CDI
 US-11-071-580-1

Query Match 19.2%; Score 398.5; DB 7; Length 444;
 Best Local Similarity 28.6%; Pred. No. 1.5e-28;
 Matches 108; Conservative 80; Mismatches 174; Indels 15; Gaps 8;

Qy 31 VAHLASDFGVRVFOQVAQASQKDRNVVFSPGVAVSLAMLOLTGGTGTQOIQAM--GF 87
 Db 75 LAKETSNFGSLRKISM-RHDGNMVFSPGMSLAMTGLMIGATGPTEQIKRGHLQAL 133
 Qy 88 KIDDKGMAPAFLRHYKELMPWNKDEBISTTDAIFYORDKLVLQGFMMPHFFRLFRSTVKQV 147
 Db 134 KPTKEPLPSLFRGLRETLSENLELSQSGFAFIHKDFDVKETPFNLSSRYFDFECVPM 193
 Qy 148 DFESEVERARFLINDWVKTHTKGMSINLUGKGAVIDQTLTRVLNVNALYFGQWKTTPFDST 207
 Db 194 NFRNASQAKRLMHNYINKETRKPKLFDI--INPETKLIVDYLFLKGMLTPDPVFT 251

Qy 208 HRRLFHKSDGSTVSYVPMMAKNTMTRLPRLLVPKFESLETEVDLRKPLENUGMTDMFQFQ 326
 Db 252 EVDTFHLDKYTKTIVKPMYMGKF---ASFDKNFRCHVULKLPYQGNATMLVVVL-MBK 305
 Qy 267 EVPLSALTNIISQALISHWKGNMTRLPRLLVPKFESLETEVDLRKPLENUGMTDMFQFQ 326
 Db 306 MGDHLAEDYLTLDVETWLNMKTRNMEVFPFKFLDKQYEMHELLRQNGIRRFFSP- 364
 Qy 327 ADFTSLS-DQEPLHVAQALQKVIEYNESGTVASSSTAVIVSARMAPEEIMDRPLFLVV 385
 Db 365 ADLSELSATGRNLQVSRLQRTVIEDERGTEAVAGILSEETAYSMPVTKVDRPFFMI 424
 Qy 386 RHNPPTGTVLFLMCOVMEP 402
 Db 425 YEETSGMFLFLGRVNP 441

RESULT 10
 US-10-131-836A-498
 Sequence 498, Application US/10131826A
 Publication No. US20050245730A1
 GENERAL INFORMATION
 APPLICANT: Baker, Kevin P.
 APPLICANT: Desnoyers, Laura
 APPLICANT: Beresini, Maureen
 APPLICANT: deForg, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Gowdribi, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.
 APPLICANT: Tomas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEARIC ACIDS ENCODING THE SAME
 FILE REFERENCE: P3340R1C128
 CURRENT APPLICATION NUMBER: US/10/131,826A
 CURRENT FILING DATE: 2002-04-24
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059124
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO: 498
 LENGTH: 444
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-131-826A-498

Query Match 19.0%; Score 394.5; DB 6; Length 444;
 Best Local Similarity 28.4%; Pred. No. 3.4e-28;
 Matches 107; Conservative 81; Mismatches 174;
 Indels 18; Gaps 8;

Qy 31 VAHLASDFGVRVFOQVAQASQKDRNVVFSPGVAVSLAMLOLTGGTGTQOIQAM--GF 87
 Db 75 LAKETSNFGSLRKISM-RHDGNMVFSPGMSLAMTGLMIGATGPTEQIKRGHLQAL 133
 Qy 31 VAHLASDFGVRVFOQVAQASQKDRNVVFSPGVAVSLAMLOLTGGTGTQOIQAM--GF 87
 Db 75 LAKETSNFGSLRKISM-RHDGNMVFSPGMSLAMTGLMIGATGPTEQIKRGHLQAL 133
 Qy 88 KIDDKGMAPAFLRHYKELMPWNKDEBISTTDAIFYORDKLVLQGFMMPHFFRLFRSTVKQV 147
 Db 134 KPTKEPLPSLFRGLRETLSENLELSQSGFAFIHKDFDVKETPFNLSSRYFDFECVPM 193
 Qy 148 DFESEVERARFLINDWVKTHTKGMSINLUGKGAVIDQTLTRVLNVNALYFGQWKTTPFDST 207
 Db 194 NFRNASQAKRLMHNYINKETRKPKLFDI--INPETKLIVDYLFLKGMLTPDPVFT 251

Query Match 19.0%; Score 394.5; DB 6; Length 444;
 Best Local Similarity 28.4%; Pred. No. 3.4e-28;
 Matches 107; Conservative 81; Mismatches 174;
 Indels 18; Gaps 8;

Qy 88 KIDDKGMAPAFLRHYKELMPWNKDEBISTTDAIFYORDKLVLQGFMMPHFFRLFRSTVKQV 147
 Db 134 KPTKEPLPSLFRGLRETLSENLELSQSGFAFIHKDFDVKETPFNLSSRYFDFECVPM 193
 Qy 148 DFSEVERARFLINDWVKTHTKGMSINLUGKGAVIDQTLTRVLNVNALYFGQWKTTPFDST 207
 Db 194 NFRNASQAKRLMHNYINKETRKPKLFDI--INPETKLIVDYLFLKGMLTPDPVFT 251
 Qy 208 HRRLFHKSDGSTVSYVPMMAKNTMTRLPRLLVPKFESLETEVDLRKPLENUGMTDMFQFQ 326
 Db 252 EVDTFHLDKYTKTIVKPMYMGKF---ASFDKNFRCHVULKLPYQGNATMLVVVL-MBK 305
 Qy 267 EVPLSALTNIISQALISHWKGNMTRLPRLLVPKFESLETEVDLRKPLENUGMTDMFQFQ 326
 Db 306 MGDHLAEDYLTLDVETWLNMKTRNMEVFPFKFLDKQYEMHELLRQNGIRRFFSP- 364
 Qy 327 ADFTSLS-DQEPLHVAQALQKVIEYNESGTVASSSTAVIVSARMAPEEIMDRPLFLVV 385
 Db 365 ADLSELSATGRNLQVSRLQRTVIEDERGTEAVAGILSEETAYSMPVTKVDRPFFMI 424
 Qy 386 RHNPPTGTVLFLMCOVMEP 402
 Db 425 YEETSGMFLFLGRVNP 441

RESULT 11
 US-10-821-234-1458

Sequence 1458, Application US/10821234
 Publication No. US20030255114A1
 APPLICANT: Labat, Ivan
 APPLICANT: Stache-Crain, Birgit
 APPLICANT: Andarmani, Susan
 APPLICANT: Tang, Y. Tom
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 FILE REFERENCE: 821A
 CURRENT APPLICATION NUMBER: US/10/821,234
 CURRENT FILING DATE: 2004-04-07
 PRIOR APPLICATION NUMBER: US 60/462,047
 PRIOR FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 1704
 SOFTWARE: Pt_seq_genes Version 1.0
 SEQ ID NO: 14-8
 LENGTH: 500
 TYPE: PRT
 ORGANISM: Homo sapiens
 us-10-821-234-1458

Query Match 15.1%; Score 312; DB 6; Length 500;
 Best Local Similarity 26.3%; Pred. No. 1.1e-20;
 Matches 107; Conservative 74; Mismatches 162; Indels 64; Gaps 14;

Qy 11 VLGALVFGEGSAVHPPSYVAHLASDFGYRVFOQAQASK-DRNVSFSPYGVASVLM 69
 Db 141 VLGDALV-----DFSLKLYHAFSAMCKVETNAFSPSIALSLTQV 181

Qy 70 QLTGGTQQIQAAMGKIDDKGKMAPAHLVYKELMGPAHKDELSITDAIFQDRLKLV 129
 Db 182 LLGAGENTKTNLESLLSPKDFTCVHQALK-----GFTIKGTVTSVSQLFHSDLAIR 233

Qy 130 QGFMPHFFRLFRSTVKQVDFBEVERARFIINDWVCHTKRMIISNLGKAVGDQLTRVLV 189
 Db 234 DTFV-NASTLYSSPRVLNSINSDANLLEINTWAKNTNNKISLSDLPSD-TTRVLV 290

Qy 190 NAYFNGQWKTPFPDSSTRHLFLHKSDGSTVSPMMAOTNKFNFTBFTPDGHYYD---- 245
 Db 291 NAYUSAKWKTIDPKKTRMFPFKN-SVVKPM---NSKKY----PVAHFIDQTLK 341

Qy 246 ---ILFLPYHDGTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRL----PRL 295
 Db 342 ARVGQOLQSHN--LSLVILVQPNLKHRLMEDMEQALSP---SVFRAIMBKLEMSKFQPTL 395

Qy 296 LVLPKESLETEDVLRKPLENIGMTDMFRQPADFTSLSDQEPHLVIAQALOKVKVEVNESG 355
 Db 396 LTLPRKVTSQDMLSIMKEEFFDF--SVDLNLCGLTEDPDQVSAMQHQTVELTETG 453

Qy 356 TVASSSTAVIVSARMAPERLIMDRPELFYVRHNHPTGTFLMGQYMEP 402
 Db 454 VERRAAASATISVARTLUVFV-QQPFELFLMLWDQQHKFPVMGRVTDP 498

RESULT 12
 Sequence 187, Application US/11186284
 Publication No. US200526643A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals, Inc.
 APPLICANT: Berger, Alison
 APPLICANT: Guillemette, Tracy L.
 APPLICANT: Kamarkar, Shubhangi
 APPLICANT: Schlegel, Robert
 APPLICANT: Monahan, John E.
 APPLICANT: Thibodeau, Stephen N.
 APPLICANT: Burgert, Lawrence J.
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TREATMENT OF COLON CANCER
 FILE REFERENCE: MPM01-029PRNM
 CURRENT APPLICATION NUMBER: US/11/186,284
 CURRENT FILING DATE: 2005-07-21

PRIOR APPLICATION NUMBER: US/10/301,822
 PRIOR FILING DATE: 2002-11-21
 PRIOR APPLICATION NUMBER: US 60/339,971
 PRIOR FILING DATE: 2001-12-10
 PRIOR APPLICATION NUMBER: US 60/361,978
 PRIOR FILING DATE: 2002-03-05
 PRIOR APPLICATION NUMBER: US 60/381,988
 PRIOR FILING DATE: 2002-05-20
 NUMBER OF SEQ ID NOS: 228
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 187
 LENGTH: 418
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-186-284-187

Query Match 14.9%; Score 308.5; DB 7; Length 418;
 Best Local Similarity 24.1%; Pred. No. 1.7e-20;
 Matches 80; Mismatches 212; Indels 17; Gaps 8;

Qy 3 MSPALTCUVLGLAVLWGECSAVHHP-SYVAHLASDFGYRVFOQAQSKDNRNFSPY 60
 Db 13 LEAALAAEYVKPAAAAPTAEKLSPKATLAERSAGLAFLSLYQAMAKDQAVENILVSEV 72

Qy 61 GVASYLAMIQLQTGGTQQIQAAMGK-F-KIDDKGMAPALHVYKELMGPMWNKEISTT-- 117
 Db 73 WVASSLGSLLGGKATTASOAKAVISAQOLRDREVHGAGELPLS--NSTARNVTK 129

Qy 118 --DAIFVORDKLVYQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVTKHTKCMISNL 175
 Db 130 LGSRIGPSSVSFADDYFVRSKOHYNCEHSKINFRKRPQSQINEWAAQTIDCKLPVTT 189

Qy 176 GKGAQDQLTRPLVIVNALLYNGQKTPFPDSSTHRLFKSDGSTVSPMMAOTNKFNFT 235
 Db 190 KD--VERTDGALLYNAMFFKPHNDEKFHKMVNDNGFMVTRSYGVMMMHRTGLNYD 247

Qy 236 FTTPDGHYDILELPYHDGTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPL 295

Db 248 --DEKEKLQIVENPLAHKLSSLILMPHVE-PLEERIEKLJITKEQLKIKWMGPQKKAVYA 303

Qy 296 LVLPKESLETEDVLRKPLENIGMTDMFRQPADFTSLSDQEPHLVIAQALOKVKIEVNBSG 355

Db 304 ISLPQGVVEYTHDQKHLAGLGLTEAIDKNAKDLRSRMGKDKLYLASVPHATAFELDTG 363

Qy 356 TVASSSTAVIVSARMAPERLIMDRPELFYVRHNHPTGTFLMGQYMEP 402
 Db 364 NPFDODIYGREELR-SPKLFYADHPFILYRDTQSGLLFIGRLVRP 409

RESULT 13
 US-10-821-234-1331
 Sequence 1331, Application US/10821234
 GENERAL INFORMATION:
 APPLICANT: Labat, Ivan
 APPLICANT: Andarmani, Susan
 APPLICANT: Stache-Crain, Birgit
 APPLICANT: Tang, Y. Tom
 APPLICANT: Andarmani, Susan
 FILE REFERENCE: 821A
 CURRENT APPLICATION NUMBER: US/10/821,234
 PRIOR APPLICATION NUMBER: 821A
 CURRENT FILING DATE: 2004-04-07
 PRIOR FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 1704
 SOFTWARE: Pt_seq_genes Version 1.0
 SEQ ID NO: 1331
 LENGTH: 418
 ORGANISM: Homo sapiens
 US-10-821-234-1331

Query Match 14.7%; Score 305; DB 6; Length 418;

Best Local Similarity 23.7%; Pred. No. 3.4e-20;
 Matches 94; Conservative 87; Mismatches 189; Indels 26; Gaps 10;

Qy 15 ALVFGEGSAVHHPSPYVAHLASDFGVRVFOOQAQSQRDNVFSPYGVASVAMILQLTG 74
 Db 38 ALVEEDDPFFKVPVNKLAAAVNSFGYDLYRVSSTSPTNVILSPLSVATALSALSIGE 97

Qy 75 GETQQOIQAMGFKIDDKGMAPALRHLYKELMGPMN --KDEIYSTDAIFQDLKLVQGF 132
 Db 98 QRTESTIHRALLY--DISSPDIHGTYKELLDVTATQNLKSASRIVFEKLRIKSF 154

Qy 133 MPHFFRLRSTVK ----QVDFSEVERARFLINDWVKTHTKGMSNLGKGAVIDQTLR 186
 Db 155 VAPLEKSYGTRPRVLGNPRLDQE----INNNWQAOQMKGLARST-KBIPDEIS-I 205

RESULT 15
 US-11-010-874-18
 ; Sequence 18, Application US/11010874
 ; Publication No. US20050250694A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ma, Jian-Xing
 ; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND FIBROSIS AND METHODS OF MAKING AND USING SAME
 ; FILE REFERENCE: 5820_656
 ; CURRENT APPLICATION NUMBER: US/11/010,874
 ; CURRENT FILING DATE: 2004-12-13
 ; PRIORITY NUMBER: 10/963,115
 ; PRIORITY FILING DATE: 2004-10-12
 ; PRIORITY APPLICATION NUMBER: 60/510,620
 ; PRIORITY FILING DATE: 2003-10-10
 ; PRIORITY APPLICATION NUMBER: 60/528,647
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 18
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-010-874-18

Query Match 10.6%; score 219; DB 7; Length 362;
 Best Local Similarity 22.9%; Pred. No. 1.5e-12;
 Matches 77; Conservative 71; Mismatches 162; Indels 26; Gaps 10;

Qy 15 ALVFGEGSAVHHPSPYVAHLASDFGVRVFOOQAQSQRDNVFSPYGVASVAMILQLTG 74
 Db 38 ALVEEDDPFFKVPVNKLAAAVNSFGYDLYRVSSTSPTNVILSPLSVATALSALSIGE 97

Qy 75 GETQQOIQAMGFKIDDKGMAPALRHLYKELMGPMN --KDEIYSTDAIFQDLKLVQGF 132
 Db 98 QRTESTIHRALLY--DISSPDIHGTYKELLDVTATQNLKSASRIVFEKLRIKSF 154

Qy 133 MPHFFRLRSTVK ----QVDFSEVERARFLINDWVKTHTKGMSNLGKGAVIDQTLR 186
 Db 155 VAPLEKSYGTRPRVLGNPRLDQE----INNNWQAOQMKGLARST-KBIPDEIS-I 205

Query Match 14.7%; score 304; DB 7; Length 418;
 Best Local Similarity 23.7%; Pred. No. 4.2e-22;
 Matches 94; Conservative 87; Mismatches 189; Indels 26; Gaps 10;

Qy 15 ALVFGEGSAVHHPSPYVAHLASDFGVRVFOOQAQSQRDNVFSPYGVASVAMILQLTG 74
 Db 38 ALVEEDDPFFKVPVNKLAAAVNSFGYDLYRVSSTSPTNVILSPLSVATALSALSIGE 97

Qy 75 GETQQOIQAMGFKIDDKGMAPALRHLYKELMGPMN --KDEIYSTDAIFQDLKLVQGF 132
 Db 98 QRTESTIHRALLY--DISSPDIHGTYKELLDVTATQNLKSASRIVFEKLRIKSF 154

Qy 133 MPHFFRLRSTVK ----QVDFSEVERARFLINDWVKTHTKGMSNLGKGAVIDQTLR 186
 Db 155 VAPLEKSYGTRPRVLGNPRLDQE----INNNWQAOQMKGLARST-KBIPDEIS-I 205

Qy 187 VLNALYFNGQWKTTPDOSTSHRLFHKSDFGSTVSPMMMAQTNKFNTEFTTPDGHYDI 246
 Db 206 LLGVAHKFGQWVTKFDSRKTSLEDFYLDDEERTVRYPMMSDPKA -VIRYGLDSLSCKI 263

Query completed: December 13, 2005, 09:26:58
 Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model 1

Run on: December 13, 2005, 09:01:30 ; Search time 39 Seconds

Title: US-10-506-406-2
 Perfect score: 2071
 Sequence: 1 MQMSPAITCLVIGLALVFGEE.....FVVRHNPTGTVLFMGSQVMEP 402

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR@:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
- 1	2071	100.0	402	1 ITHUP1
2	1784	86.1	402	1 S0745
3	1746	84.3	400	2 JC4265
4	1680	81.1	402	1 A35032
5	1626	78.5	402	1 A34761
6	796.5	38.5	397	2 148717
7	791.5	38.2	2 B27496	
8	761	36.7	398	2 A37274
9	620	29.9	410	2 S70647
10	503	24.3	378	2 S38962
11	498.5	24.1	416	2 B25131
12	498	24.0	402	1 A34762
13	490	23.7	413	2 148717
14	487.5	23.5	418	2 S21675
15	486	23.5	413	2 JX0154
16	482.5	23.3	390	2 J38202
17	480	23.2	411	1 ITTR
18	480	23.2	413	2 S54981
19	479	23.1	379	2 S27283
20	479	23.1	403	2 S08102
21	476	23.0	413	2 J4973
22	474.5	22.9	464	1 XHHTU3
23	472	22.8	413	2 149472
24	470.5	22.7	465	2 159611
25	469	22.6	415	2 A32853
26	465.5	22.6	408	2 A55333
27	468	22.6	376	1 A46681
28	468	22.6	413	2 I49470
29	467.5	22.6	374	2 A59273

RESULT 1

ITHUP1

Plasminogen activator inhibitor 1 precursor [validated] - human
 N;Alternate names: Plasminogen activator inhibitor, endothelial

C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 05-Oct-2004
 C;Accession: A28107; S05551; T26996; I59126; JS0397; A25833; A26146; A29100; A25895; A25
 R;Boma, P.J.; van den Berg, B.A.; Kooistra, T.; Siemieniak, D.R.; Slichter, J.L.
 J. Biol. Chem. 263: 9129-9141, 1988
 A;Title: Human plasminogen activator inhibitor-1 gene. Promoter and structural gene nuc1
 A;Reference number: A28107; MUID:8900511; PMID:3132455
 A;Accession: A28107
 A;Molecule type: DNA
 A;Residues: 1-402 <STR>
 A;Cross-references: UNIPARC:UPI00000000CAB; GB:J03764; PIDN:9189564; PIDN:
 R;Strandberg, L.; Lawrence, D.; Ny, T.
 R;Lokutoff, D.J.; Linders, M.; Keijer, J.; Veerman, H.; van Heerikhuizen, H.; Pannekoek
 Biochemistry 26: 3763-3768, 1987
 A;Title: Structure of the human plasminogen-activator-inhibitor-1 gene. Implicati
 A;Reference number: S02551; MUID:8900511; PMID:31262512
 A;Accession: S02551
 A;Molecule type: DNA
 A;Residues: 1-14, 'T', 16-402 <STR>
 A;Cross-references: UNIPARC:UPI00001731AA; EMBL:X13338; PIDN:935244; PIDN:
 A;Note: the complete translation is not annotated in GenBank entries HSPAI11, HSPAI12, H
 R;Van Zonneveld, A.J.; Curriden, S.A.; Loskutoff, D.J.
 Proc. Natl. Acad. Sci., U.S.A., 85, 5525-5529, 1988
 A;Title: Type 1 plasminogen activator inhibitor 1 gene: nonrandom distri
 A;Reference number: A26996; MUID:88000386; PMID:2820474
 A;Accession: A26996
 A;Molecule type: DNA
 A;Residues: 1-402 <LOS>
 A;Cross-references: UNIPARC:UPI00000000CAB; GB:M2321; GB:MI7121; PIDN:9189576; PIDN:9189578; has the cod
 R;Gene 84, 447-453, 1989
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-9 <ZDN>
 A;Cross-references: UNIPARC:UPI00000003BD; GB:J03836; PIDN:9189579; MUID:90128289; PMID:2612914
 R;Pollio, M.; Ginsburg, D.
 A;Title: Structure and expression of the human gene encoding plasminogen activator inhib
 A;Reference number: JS0397; MUID:90128289; PMID:90128289
 A;Molecule type: DNA
 A;Residues: 85-86-88-93-166-171-231-236-298-302;311-336-3360-365;>88-393 <FOI>
 A;Cross-references: UNIPARC:UPI00001731AB; UNIPARC:UPI00001731AC
 1B1; GB: M33136; PID:9189543
 A;Note: sequences of the intron/exon boundaries are shown

ALIGNMENTS

R;Pannekoek, H.; Veerman, H.; Lambers, H.; Diergaardde, P.; Verveij, C.L.; van Zonneveld, EMBIO J. 5, 239-254, 1986	A;Title: Endothelial plasminogen activator inhibitor (PAI) : a new member of the serpin q	oma cells. Vascular endothelial cells may be the primary site of synthesis of plasma PAI
A;Cross-references: UNIPARC:UPI0000000CAB; GB:X04429; PIDN:CAA28025.1; PID:9	C;Comment: Glycosylation is not required for inhibitory activity.	C;Genetics:
R;Man, T.C.; Kretzmer, K.K.	A;Gene: GDB:PAII; PLANH1	A;Gene: GDB:PAII; PLANH1
FBSB Lett. 20, 11-16, 1987	A;Cross-references: GDB:120297; OMIM:1733360	A;Cross-references: UNIPARC:UPI00001731B3; UNIPARC:UPI00001731B4
A;Title: cDNA cloning of human plasminogen activator-inhibitor from endothelial cells.	A;Map position: 7q21.3-7q22	R;Kjoller, L.; Martensen, P.M.; Sottrup-Jensen, L.; Justesen, J.; Rodenburg, K.W.; Andre
A;Reference number: A91052; MUID:87053819; PMID:2430793	A;Introns: 9/1; 16/1; 234/1; 300/2; 334/1; 363/1; 391/1	Biochem. Biophys. Acta 1295, 103-109, 1996
A;Accession: A25693	C;Superfamily: serpin	A;Title: Conformational changes of the reactive-centre loop and beta-strand 5A accompany
A;Residues: 1-402 <PAN>	C;Keywords: glycoprotein; serine proteinase inhibitor	A;Reference number: S74133; MUID:97054589; PMID:889886
A;Cross-references: UNIPARC:UPI0000000CAB; GB:X04429; PIDN:CAA28025.1; PID:9	F;1-23/Domain: signal sequence #status predicted <SIG>	A;Accession: S74133
R;Ginsburg, D.; Zelena, R.; Yang, A.Y.; Rafferty, U.M.; Andreassen, P.A.; Nielsen, L.; Dan	F;1-24-402/Product: Plasminogen activator inhibitor-1 #status experimental <MAT>	A;Molecule type: protein
J. Clin. Invest. 78, 1673-1680, 1986	F;232/288/352/Binding site: carbohydrate (Asn) (covalent) #status predicted	A;Cross-references: UNIPARC:UPI00001731B3; UNIPARC:UPI00001731B4
A;Title: cDNA cloning of human plasminogen activator-inhibitor from endothelial cells.	F;369/Inhibitory site: Arg (plasminogen activator) #status predicted	R;Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
A;Reference number: A92166; MUID:87058123; PMID:3097076	A;Molecule type: mRNA	C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:URK01
A;Accession: A26146	A;Residues: 1-402 <GIN>	Eur. J. Biochem. 176, 81-87, 1988
A;Cross-references: UNIPARC:UPI0000000CAB; GB:M16006; NID:9189541; PIDN:AAA60003.1; PID:9	A;Cross-references: UNIPARC:UPI0000000CAB; GB:X0744; NID:935275; PIDN:CAA28444.1; PID:9	C;Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339).
R;Man, T.C.; Kretzmer, K.K.	A;Note: Part of this sequence, including the amino end of the mature protein, was confirm	A;Title: Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induc
FBSB Lett. 20, 11-16, 1987	R;NY, T.; Saudek, M.; Lawrence, D.; Millan, J.L.; Loskutoff, D.J.	A;Accession: A29100; MUID:87105025; PMID:3026337
A;Title: cDNA cloning and expression in E. coli of a plasminogen activator inhibitor (PAI)	Proc. Natl. Acad. Sci. U.S.A. 83, 6776-6780, 1986	A;Molecule type: mRNA
A;Reference number: A29100; MUID:87105025; PMID:3026337	A;Title: Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-	A;Cross-references: UNIPARC:UPI00001423AD; GB:M14083; NID:9189566; PIDN:AAA60008.1; PID:9
A;Accession: A29100	A;Reference number: A25895; MUID:86313660; PMID:3092219	R;Andreassen, P.A.; Riccio, A.; Weinder, K.G.; Douglass, R.; Sartorio, R.; Nielsen, L.S.;
A;Molecule type: mRNA	A;Molecule type: mRNA	FBSB Lett. 209, 213-218, 1986
A;Residues: 1-402 <NTY>	A;Residues: 1-14, "T", 16-47 <AND1>	A;Title: Plasminogen activator inhibitor type-1: reactive center and amino-terminal hete
A;Cross-references: UNIPARC:UPI00001423AD; GB:M14083; NID:9189566; PIDN:AAA60008.1; PID:9	A;Accession: A25651	A;Reference number: A91371; MUID:87080762; PMID:3025016
R;Andreassen, P.A.; Riccio, A.; Weinder, K.G.; Douglass, R.; Sartorio, R.; Nielsen, L.S.;	A;Molecule type: mRNA	A;Molecule type: mRNA
FBSB Lett. 209, 213-218, 1986	A;Residues: 1-14, "T", 16-47 <AND1>	A;Residues: 1-14, "T", 16-47 <AND1>
A;Title: Plasminogen activator inhibitor type-1: reactive center and amino-terminal hete	A;Cross-references: UNIPARC:UPI000016AESC; GB:X04729; NID:935263; PIDN:CAA28438.1; PID:9	A;Cross-references: UNIPARC:UPI000016AESB; GB:X04731; NID:935260; PIDN:CAA28442.1; PID:9
A;Reference number: A91371; MUID:87080762; PMID:3025016	A;Accession: B25651	R;Laug, W.E.; Aebersold, R.; Jong, A.; Rideout, W.; Bergman, B.L.; Baker, J.
A;Accession: A25651	A;Molecule type: mRNA	The comb. Haemost. 61, 517-521, 1989
A;Residues: 1-44-402 <AND2>	A;Residues: 1-14, "T", 16-47 <AND1>	A;Title: Isolation of multiple types of plasminogen activator inhibitors from vascular s
A;Cross-references: UNIPARC:UPI000016AESB; GB:X04731; NID:935260; PIDN:CAA28442.1; PID:9	A;Cross-references: UNIPARC:UPI00001731B2	A;Reference number: S74133; MUID:90020174; PMID:2799763
R;Laug, W.E.; Aebersold, R.; Jong, A.; Rideout, W.; Bergman, B.L.; Baker, J.	R;Kjoller, L.; Martensen, P.M.; Sottrup-Jensen, L.; Justesen, J.; Rodenburg, K.W.; Andre	A;Accession: A60436
The comb. Haemost. 61, 517-521, 1989	Biochem. Biophys. Acta 1295, 103-109, 1996	A;Molecule type: protein
A;Title: Isolation of multiple types of plasminogen activator inhibitors from vascular s	A;Title: Characterization of the complex of plasminogen activator inhibitor type 1 with	A;Residues: 22-30; 370-376 <KJO>
A;Reference number: A60436; MUID:90020174; PMID:2799763	A;Title: Conformational changes of the reactive-centre loop and beta-strand 5A accompany	A;Cross-references: UNIPARC:UPI00001731B3; UNIPARC:UPI00001731B4
A;Accession: S74133	A;Reference number: S74133; MUID:97054589; PMID:889886	R;Stroemavist, M.; Karlsson, K.E.; Bjoerquist, P.; Andersson, J.O.; Bystroem, M.; Hansso
A;Molecule type: preliminary	A;Accession: S70346	Biochem. Biophys. Acta 1295, 103-109, 1996
A;Residues: 22-30; 370-376 <STO>	A;Accession: S70346	A;Title: Characterization of the complex of plasminogen activator inhibitor type 1 with
A;Cross-references: UNIPARC:UPI00001731B3	A;Accession: S70346; MUID:96283799; PMID:96283799	A;Reference number: S70346; MUID:96283799; PMID:96283799
R;Kjoller, L.; Martensen, P.M.; Sottrup-Jensen, L.; Justesen, J.; Rodenburg, K.W.; Andre	A;Accession: S70346	A;Molecule type: protein
Biochem. Biophys. Acta 1295, 103-109, 1996	A;Accession: S70346	A;Cross-references: UNIPARC:UPI00001731B5
A;Title: Conformational changes of the reactive-centre loop and beta-strand 5A accompany	A;Accession: S70346	R;Pepper, M.S.; Belin, D.; Montesano, R.; Orci, L.; Vassalli, J.D.
A;Reference number: S74133; MUID:97054589; PMID:889886	A;Accession: S70346	J. Cell Biol. 111, 743-755, 1990
A;Accession: S74133	A;Accession: S74133	Nucleic Acids Res. 17, 8872, 1989
A;Molecule type: protein	A;Accession: S74133	A;Title: CDNA for bovine type I plasminogen activator inhibitor (PAI-1).
A;Residues: 1-402 <NTY>	A;Accession: S74133	A;Reference number: S06745; MUID:90067867; PMID:2587231
A;Cross-references: UNIPARC:UPI00001731B2	A;Accession: S74133	A;Molecule type: mRNA
R;Kjoller, L.; Martensen, P.M.; Sottrup-Jensen, L.; Justesen, J.; Rodenburg, K.W.; Andre	A;Accession: S74133	A;Cross-references: UNIPROT:P13909; UNIPARC:UPI00002FBA6; EMBL:X16383; NID:9600; PIDN:CA
Biochem. Biophys. Acta 1295, 103-109, 1996	A;Accession: S74133	C;Species: Bos primigenius taurus (cattle)
A;Title: Characterization of the complex of plasminogen activator inhibitor type 1 with	A;Accession: S06745	C;Accession: S06745; S01324; S10906
A;Reference number: S74133; MUID:97054589; PMID:889886	A;Accession: S74133	R;Mimuro, J.; Sawaya, M.; Hattori, M.; Luskutoff, D.J.
A;Accession: S70346	A;Accession: S70346	Nucleic Acids Res. 17, 8872, 1989
A;Molecule type: protein	A;Accession: S70346	A;Title: CDNA for bovine type I plasminogen activator inhibitor (PAI-1).
A;Residues: 22-30; 370-376 <STO>	A;Accession: S70346	A;Reference number: S06745
A;Cross-references: UNIPARC:UPI00001731B5	A;Accession: S70346	A;Molecule type: mRNA
R;Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.	A;Accession: S70346	A;Cross-references: UNIPARC:UPI000016C357; EMBL:X52306; NID:9598; PIDN:CAA37094.1; PID:9598
C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:URK01	A;Accession: S70346	C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:URK01
Eur. J. Biochem. 176, 81-87, 1988	A;Accession: S70346	Eur. J. Biochem. 176, 81-87, 1988
C;Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339).	A;Accession: S70346	A;Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and heat e

RESULT 2

S06745

Plasminogen activator inhibitor-1 precursor - bovine

N;Alternate names: endothelial-cell plasminogen activator inhibitor; PAI-1

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Feb-1990 #text_change 05-Oct-2004

C;Accession: S06745; A35855

R;Mimuro, J.; Sawaya, M.; Hattori, M.; Luskutoff, D.J.

Nucleic Acids Res. 17, 8872, 1989

A;Title: CDNA for bovine type I plasminogen activator inhibitor (PAI-1).

A;Reference number: S06745; MUID:90067867; PMID:2587231

A;Molecule type: mRNA

A;Residues: 1-402 <MM>

A;Cross-references: UNIPROT:P13909; UNIPARC:UPI00002FBA6; EMBL:X16383; NID:9600; PIDN:CA

C;Species: Bos primigenius taurinus (cattle)

C;Accession: S06745; S01324; S10906

R;Pepper, M.S.; Belin, D.; Montesano, R.; Orci, L.; Vassalli, J.D.

J. Cell Biol. 111, 743-755, 1990

A;Title: Transforming growth factor-beta 1 modulates basic fibroblast growth factor-induc

A;Reference number: A35855; MUID:90338128; PMID:1692667

A;Accession: A35855

A;Molecule type: protein

A;Cross-references: UNIPARC:UPI000016C357; EMBL:X52306; NID:9598; PIDN:CAA37094.1; PID:9598

C;Comment: This inhibitor acts as "bait" for tissue plasminogen activator (see PIR:URK01

Eur. J. Biochem. 176, 81-87, 1988

C;Comment: Three types of PAI have been identified (see also PIR:A32853 and PIR:A39339).

A;Residues: 24-43, 'G' <OVS>
A;Cross-references: UNIPARC:UPI00001731B7
C;Genetics: A;Introns: 91/1; 169/1; 234/1; 300/2; 334/1; 363/1; 391/1
C;Superfamily: serpin
C;Keywords: glycoprotein
P;1-23/Domain: signal sequence #status predicted <SIG>
P;24-402/Product: plasminogen activator inhibitor-1 #status experimental <MAT>
P;24-402/Product: carbohydrate (Asn) (covalent) #status predicted
P;363/Inhibitory site: Arg (plasminogen activator) #status predicted

Query Match 81.1%; Score 1680; DB 1; Length 402;
Best Local Similarity 80.8%; Pred. No. 1..5e-124;
Matches 325; Conservative 36; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MQMSPALTCLVGLALVFGEGSAVTHPPSYVAHLASDFGYRVFQQVAQASKDRNNUFSFY 60
Db 1 MQMSSALTCATLGLIVFGKFAPLPESTAAQQTINFGKVVFQHVAQSKDRNNUFSFY 60

Qy 61 GVASYLAMILQLTTGGETTOQIQAANGFKIDKGMAPALRHLYKELMGPNKDETISTTDI 120
Db 61 GVSSYLMAMILQLTTGKTRQQIDANGENISERGTAPALRKLSEKLMGSWINKNEISTADI 120

Qy 121 FVQDILKLVQGFMPIFFKPLRSTYKQVDSEVERARFININDWVTKTICGMISNLGKAV 180
Db 121 FVQDILKLVQGFMPIFFKPLRSTYKQVDSEVERARFININDWVTKTICGMISDLAKAV 180

Qy 181 DQLTRVLVNLALYFNGQWKTTPFDSSTHRFLHKSDGSTSVPMMAQTNKFNNTBEFTTD 240
Db 181 NELTRVLVNLALYFNGQWKTTPFLEASTHQLFLHKSDGSTSVPMNAQNKKFNNTBEFTTD 240

Qy 241 GHYYDILELPYHGDTLSMFIAPYKEVPLSALTNLISQLISHWKGNTRLPRLLVFK 300
Db 241 GHEYDILELPYHGDTLSMFIAPFDPVPSAITMILDAILRQWKSNNTRLPPLLIFK 300

Qy 301 FSLETEVDLKRPLENGLMTDMFQOAFDTSLSDOPLHYAQALOKVKIEVNESGTVAASS 360
Db 301 FSLETEVDLQRPLEKIGMTDIFSSTQADFSLSDOQELQSVAAQALOKVKIEVNESGTVAASS 360

Qy 361 STAVIVSARMAPAEITIMDRPFLTVRNPPTGTVLFMGQYMEP 402
Db 361 STAVIVSARMAPTEMVIRSFLVVRNPETILFMGQYMEP 402

RESULT 6
Db 14817 proteinase inhibitor nexin I precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 05-Oct-2004
C;Accession: I48717; S70772; S35731
R;Yassallil, J.D.; Huarte, J.; Bosco, D.; Sappino, A.P.; Velardi, A.; Wohlwein
EMBO J. 1, 1871-1878, 1993
A;Title: Protease-nexin I is an androgen-dependent secretory product of the murine seminiferous tubule
A;Reference number: I48717; MUID: 93259128; PMID: 8491179
A;Accession: I48717
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-397 -RES,
A;Cross-references: UNIPROT:Q07235; UNIPARC:UPI0000004078; EMBL:X70296; NID:9551064; PID:
A;Statue: nucleic acid sequence not shown, translation not shown
A;Molecule type: DNA
A;Residues: 1-86 <VAS>
A;Cross-references: UNIPARC:UPI00016CFC8; EMBL:X70946; NID:957930; PID:CAA50285_1; PID:
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993
C;Genetics:

A34761 C;Superfamily: serpin
C;Keywords: serine proteinase inhibitor
P;1-19/Domain: signal sequence #status predicted <SIG>
P;20-39/Domain: proteinase inhibitor nexin I #status predicted <MAT>

Query Match 38.5%; Score 796.5; DB 2;
Best Local Similarity 43.0%; Pred. No. 5..5e-55;
Matches 159; Conservative 74; Mismatches 134; Indels 3; Gaps 2;

Qy 34 LASDGFGRVFGQVQAQSKDRNNUVPSGVASVAMLOLTGGTGTQOAMGFKIDDKG 93
Db 30 LGSGNTGIVFQNQIKSRPHENVVPHGIASTLGMLOQGADGKTKQUSTVNRYNN-G 87

Qy 94 MAPALRHLYKELMGPNKDEISTTDIATVQDILKLVQGFMPIFFRPLFRSTVKOYDFSEVE 153
Db 88 VGRVLLKCINKAIKSVKNDIVTVANAVLRGKMEVPAVRNKKDVOCEQNTNFQDPA 147

Qy 154 RAREFLINDWVKTHTKGMISNLGKAVD-QLTRVLVNLALYFNGQWKTDPFDPDSSTHRLF 212
Db 148 SASPSINFVVKNETRGMFDNLSPNLDGALTRVLVNAVYFKGLWSRFQEPSTKRTF 207

Query Match 78.5%; Score 1626; DB 1; Length 402;
Best Local Similarity 78.6%; Pred. No. 2..7e-120;
Matches 316; Conservative 41; Mismatches 45; Indels 0; Gaps 0;

Qy 213 HKSDGSTSVPMMAQTNKFNNTBEFTPDGHYDILELPYHGDTSMLFIAAPYEKEVPLSLA 272

30 LGSDTGQVFNQIIKQSOPHENVVISPHGIAISILGMQLQGADGRTKQKLSTVMRYNVN--G 87
 94 MAPALRHLYKELMGMFWNKDEISTDTDAIFYORDLKVUQGFMPMFPRFLFRETVKQVDFSEVE 153
 94 :
 88 VGVKVRKINKAIVSKNNDLVTVANAVFVRNGFKEVPPAARNKEVFQCEVQSVNFQDPA 147
 154 RARFLINDAVKTKTAKGMISNLKGKAVDQ-LTRLVLYNVALYFGNCWKTPEPDSSSTHRLF 212
 148 SACDINFVWQNENETGMIDNLSPNLSALTSPLTQEPNKRTF 207
 148 :
 Db 208 VAGDGKSYQVPMLAQLSVRSGSTRTPGLWYNFIELPVGEISIIMLALPTESSTPLSA 267
 Qy 273 LTNILSAQLQKVKIEVNESGTVASSSTAVIVSARMAPAEIIMDRPFLFVVRHNPTGT 392
 Db 268 IIPHITKTINSWMTMVKRMOLLPKFTALAQTDLKEPLKALITMEMEPSKANFAKI 327
 Qy 333 SDQEPIHVQAQLQKVKIEVNESGTVASSSTAVIVSARMAPAEIIMDRPFLFVVRHNPTGT 392
 Db 328 TRSESSHVSHLQRKAKIEVBGDTAAVWTAILARSSPPWFIVDRPFLFCIRNPTGA 387
 Qy 393 VLFGMGOVMEP 402
 Db 388 ILFLGQVNP 397

RESULT 7
 B27496 Proteinase inhibitor nexin 1 precursor - rat (fragment)
 N; Alternate names: glia-derived nexin (CDN)
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Oct-2004
 C; Accession: B27496; A42358; B42351; C42351;
 R; Sommer, J.; Gloer, S.M.; Rovelli, G.F.; Hofsteenge, J.; Nick, H.; Meier, R.; Monard, D.
 Biochemistry 26, 6407-6410, 1987
 A; Title: cDNA sequence coding for a rat glia-derived nexin and its homology to members of
 A; Reference number: A90519; MUID:8810754; PMID:8810754; PID:9204283
 A; Accession: B27496
 A; Molecule type: mRNA
 A; Residues: 1-397 <SOM>
 A; Cross-references: UNIPARC:PO7092; UNIPARC:UPI000002BDD0; GB:MI17784; NID:9204283; PIDN:
 A; Note: the authors translated the codon TGG for residue 156 as Thr
 R; Nick, H.; Hofsteenge, J.; Gloer, S.; Rovelli, G.; Monard, D.
 Biochemistry 29, 2417-2421, 1990
 A; Title: Functional sites of glia-derived nexin (CDN): importance of the site reacting w
 A; Reference number: A34538; MUID:90248459; PMID:2337608
 A; Accession: A34538
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 364-394 <NIC>
 A; Molecule type: protein
 A; Residues: 82-96 <ROV1>
 A; Cross-references: UNIPARC:UPI00000E761E
 Biochemistry 31, 3542-3549, 1992
 A; Note: sequence extracted from NCBI backbone (NCBIP:93846)
 A; Accession: B42351
 A; Molecule type: protein
 A; Cross-references: UNIPARC:UPI000005D4A
 A; Note: sequence extracted from NCBI backbone (NCBIP:93851)
 A; Accession: C42351
 A; Molecule type: protein
 A; Residues: 317-333 <ROV2>
 A; Cross-references: UNIPARC:UPI000005BSB74
 A; Note: sequence extracted from NCBI backbone (NCBIP:93856)
 A; Note: peptide sequences were determined from rat cDNA cloned and expressed in yeast
 C; Superfamily: serpin
 C; Keywords: glycoprotein; serine proteinase inhibitor
 P 1-20/Domain: signal sequence #status predicted <SIG>
 P 21-39/Product: proteinase inhibitor nexin 1 #status predicted
 P 159/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 38.2%; Score 791.5; DB 2; Length 397;
 Best Local Similarity 42.7%; Prod. No. 4.1e-54;
 Matches 158; Conservative 72; Mismatches 137; Indels 3; Gaps 2;
 Qy 34 LASDFGVRYFQQAQASIKDRNTVYFSPYGVASVTLMLQTTGGCTQQO1QAANGFKIDKG 93

Db	298 GS-RADLTGMSEARDLFISKVHKSFVEVNEEGTEAAATXGIAVFAMLMPEDFIADHP	356	A;Residues: 1-69, 'C', 71-72, 'A', 74-193, 'D', 195-249, 'V', 251-384, 'V', 386-416 <KOR> A;Cross-references: UNIPARC:UPI00001762F5 C;Generic: 8 A;Introns: 211/1; 302/2; 352/3 C;Superfamily: serpin C;Keywords: glycoprotein; serine proteinase inhibitor
Qy	381 FLTVVRHNPSTGTVLFGMQLMEP	402	Query Match 24.1%; Score 498.5; DB 2; Length 416; Best Local Similarity 30.2%; Pred. No. 1..7e-31; Gaps 10; Matches 120; Conservative 94; Mismatches 154; Indels 29; Gaps 10;
Db	357 FIFFIRHNPPSSNLLFLGRSSP	378	19 GEGSAVHHPPTSYAHLASDFGVRFVQQAQASKDRNVSFSPYCVASVIALMLQITGGTGTQ 78 35 GKGRLH--SLTLASINTDFTLSLYKLALRNPDVKVFSPLSISAAALISLGAKDSTM 92
			79 QQIQAMGP--KIDDKGKMAPALRHLYKELMGWPKNDLTSITDAIFVDRDLKLVQGFMPH 135 93 EETILEGLKEPNLTETEEIHQGFLHLLRLSQPDQAEINTGSALFIDEQPIUSEFOEK 152
			136 FFRRLRSTVQVDPSEVERBARFFINDWYKTHTKGMISNLGKAVDQLTRVLVNALYN 195
			153 TRALYQAEAFVADEPKQCNNEAKKFINDYVSNOTQKIAELFSE--LDERTSMVLYNLLFK 210
			Db 196 GQWTPFPDSSTHRLFKHSGDGSTSVPMMAQTQNFKNTBFFTP----DGHYDILELPY 251
			93 252 HGDPLSMEFAAPYKEVPUSALTNLSAQILSHWKGNTRPLP---LVLPKFELETEVD 308
			Db 265 TGNASALFILPDQSK--MQQVESSLQPTTLKWKWDSL--PRISELEMPKFSTSTDIN 319
			267 309 LRKPLBNLGNMTDMPRQFDQFTSLSDQEPLHVAQALQRKIEVNESGTYASSSTAVIVSA 368
			320 LEEVIFELGIRKTSQ-QADLSRSITGTKNLHVQSVVHKAVIDVDFGTGAAATPAVTAA 378
			369 RMAPPEIIM---DRFLFVVRHNPNTGTVLFMGQWMP 402
			379 KSLPDTIPLNFNRPFMLVITDNNGQSVPFMGRYTNP 415
			RESULT 12
			A42421 leucocyte elastase inhibitor - horse
			N;Alternate names: Plasminogen activator inhibitor-2 homolog
			C;Species: Equus caballus (domestic horse)
			C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 05-Oct-2004
			C;Accession: A42421; A3776; S34062
			R;Dubin, A.; Travis, J.J.; Engild, J.J.; Potempa, J.
			J. Biol. Chem. 267, 6575-6583, 1992
			A;Title: Equine leucocyte elastase inhibitor. Primary structure and identification as a
			A;Reference number: A42421; PMID:1551869
			A;Accession: A42421; MURD:3220200; PMID:3220200
			A;Molecule type: protein
			A;Status: preliminary
			A;Residues: 1-41, 'E', 43-325, 'VD', 326-379 <DUB2>
			A;Cross-references: UNIPARC:UPI000012D513; PIDN:AAB21885.1; PMID:9247842
			A;Experimental source: leukocyte
			A;Note: sequence extracted from NCBI backbone (NCBIP:89849)
			R;Ohkubo, K.; Ogata, S.; Misumi, Y.; Takami, N.; Ikebara, Y.
			J. Biochem. 109, 243-250, 1991
			A;Title: Molecular cloning and expression of an intracellular serpin: an elastase inhibitor
			A;Reference number: S34062; PMID:9331957; PMID:7687138
			A;Accession: S34062
			A;Status: preliminary
			A;Molecule type: mRNA
			A;Residues: 1-379 <KOR>
			A;Molecule type: DNA
			A;Accession: A37889
			A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
			A;Molecule type: mRNA
			A;Residues: 1-49 <CH2>
			A;Cross-references: UNIPARC:UPI00001762F4
			R;Chao, J.; Chai, K.X.; Chen, L.M.; Xiong, W.; Chao, S.; Woodley Miller, C.; Wang, L.; 1
			J. Biol. Chem. 265, 16394-16401, 1990
			A;Title: Tissue kallikrein-binding protein is a serpin. Purification, characterization,
			A;Reference number: A37889; PMID:90375506; PMID:2398056
			A;Accession: A37889
			A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
			A;Molecule type: DNA
			A;Accession: A37889
			A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
			A;Molecule type: mRNA
			A;Accession: A37889
			A;Status: preliminary
			A;Molecule type: mRNA

Qy	91 DKGMA---PALRHYKELMGPNWKDEISSTDALFVORDLKLVQGMPHFFRLFRSTVKQV 147	Db	366 AAGATYMEIIPMSLPPDSITLDRPEFLVIYSHEIKSPLFVGKVVDP 410
Db	107 ETSEADIHQGFGHLLORLSQEDQDGINGRAMFLERDQLLAEPHEKABALIQTEAFTA 166		Search completed: December 13, 2005, 09:11:41 Job time : 40 secs
Qy	148 DFEVERARPKINDWVKTHTKGIMSNULGKGAVIDQTLTRVLVNALEYNGQWKTPEPDSS 207		
Db	167 DFQKEPEAKNLINDYVSNTQGCMKELISE--LDTDTLMLVNLVNYXFGRWKISDFPQDT 224		
Qy	208 HRRLFHKSDGSTVSVPMQAQNKNYTFTPDGHYYD----ILEPLPHGDTLSMFA 261		
Db	225 FESEFYLDERSVKVPMKMK - KELTR ----HFRDEELSCSVELEKYTGNASALFIL 276		
Qy	262 APYEKEVPLSALTNLISQALSHWKGNMTRLPRLLPKESLETEVDLRKPLENLGMDDM 321		
Db	277 PPGQRMQVEA -SLOPDTLKWKWSLTKRGELYLPKSISIDNLKDLPELGKBI 334		
Qy	322 FRQFOADFTSLSDQEPLHVAQALQKVKEVNESGTVYASSSTAVIV--SARMAPEEIIIMD 378		
Db	335 FSK-QADLSGTGTGKDLVSQVHVKAVALDVATGTAAAATGFIFGRSRRLQTMTVQFN 393		
Qy	379 RPFLEVVRHNPTGTVLFMGQWEP 402		
Db	394 RPFLMVISHTGVTQTLFMAKVTNP 417		
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RESULT 15			
	JX0154		
	alpha-1-antiproteinase F - rabbit		
C;Species:	Oryctolagus cuniculus (domestic rabbit)		
C;Date:	04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 05-Oct-2004		
C;Accession:	JX0154		
R;Saito, A.; Sinochar, H.			
J;Biochem. 109, 158-162, 1991			
A;Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiproteinase F: amino acid sequence number: JX0154; MUID:91201273; PMID:2016265			
A;Accession:	JX0154		
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-413 <SAI>			
A;Cross-references: UNIPROT:P23035; UNIPARC:UPI0000124FCE; GB:X57710; NID:91455; PIDN:CA			
C;Superfamily: serpin			
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Best Local Similarity 29.9%; Pred. No. 1, 7e-30; Mismatches 175; Indels 18; Gaps 7;			
Matches 121; Conservative 91; MisMatches 175; Length 413;			
Qy	7 LTCVLGLALVFGEGSAV----HHPPSY-VAHLASDFGVRYFOQVAQASKDRNYYFSPY 60	Db	15 LGCLLPGGLADEQETAVSSHEQDHAPCHRIAPSIAEFLAFLSYREVAHESNTNNIFSPV 74
Qy	61 GVASVLANLQLTGTGETOQIQAANGFKIDDKGMA -- PALRHLKELMGPWNKDEISTT 117	Db	75 STIALFANLISLGAKGDHTQVLEGLKFLNLTETAQIHDFRHLHLLTVNRPSSELQAAAR 134
Qy	118 DALFVORDLKLVQGFMMPFFRLFRSTVKYQDFSEVERFLRFLNWDVTKHGMISNLGK 177	Db	135 NALVYHENKLQHKFLEDAKLNQSEAFLVDFPDEQAKTKINSHVEKGTRGKIVDlVQB 194
Qy	178 GAVDQLTRVLVNALEYNGQWKTPEPDSSTHRFLFKHSGSTVSPVMACNTKFNTTEFT 237	Db	195 --LDARTLIALVNVVFPCCKWEPPEPNTKEEDHYATTTVRPMMSRLGRYDLFHCS 252
Qy	238 TPDGHYYDILLEPLPHGDTLSMFAAAYPEKEVPLSALTNLISQALISHWKGNMTRLPILL 297	Db	253 TLAS--TVLMDYKGNATLFL--LDEGKQHQHLETTBLTFLAKSSLRSVTVH 306
Qy	298 LPKFSLETEVDLRKPLENLGMDDMFRQFDTSLSLQDPLVIAQALQVKLBVNNEGCTV 357	Db	307 FPKLISGTYDKELLGKGITQFSD-NADLSGITEDEPLKASQALHKAVALTIDERGTE 365
Qy.	358 ASSSTAVIVSARMAPEEETIMDRPFLPVYRHNPTGTVLFMGQYMEP 402		

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